

1	pir2.521333	+	125.50	175.58	0.0160	680	!	probable endoglucanase - Rh
2	pir2.S07132	+	123.50	170.93	0.0223	885	!	hypothetical protein 1 - Rh
3	pir2.C07550	+	116.00	166.93	0.0880	376	!	adenine deaminase-related p
4	pir2.C86985	+	115.50	167.58	0.0951	320	!	conserved hypothetical prot
5	pir2.C39135	+	115.00	164.06	0.1094	437	!	hypothetical protein 3 (gyr
6	pir2.145093	+	114.50	160.45	0.1259	603	!	hypothetical protein (impor
7	pir2.A48758	+	114.00	165.43	0.1277	314	!	conserved hypothetical prot
8	pir2.153071	+	114.00	160.19	0.1380	625	!	ucrase (EC 3.5.1.5) alpha c
9	pir2.A34615	+	113.00	159.37	0.1397	665	!	profilaggrin - rat (fragmen
10	pir2.C87627	+	113.00	156.36	0.1739	738	!	hypothetical protein CC3055
11	pir2.1442761	+	113.00	151.67	0.2165	3938	!	Bassoon protein - rat
12	pir2.138669	+	112.00	151.20	0.2234	1104	!	transcription factor NFX1
13	pir2.T114180	+	112.00	151.12	0.2239	1122	!	exit protein - Mycobacteri
14	pir2.T02345	+	112.00	147.01	0.2380	1791	!	hypothetical protein KIAA0
15	pir2.A335938	+	111.50	144.23	0.2706	2248	!	profilaggrin - human (frag
16	pir2.1471954	+	111.00	140.42	0.3233	938	!	probable Lipid A biosynthes
17	pir2.1897369	+	109.00	148.32	0.3944	913	!	translational initiation fact
18	pir2.AB2587	+	109.00	147.03	0.3944	913	!	translational initiation fact
19	pir2.1883273	+	108.00	145.99	0.4020	1057	!	ribonuclease E PA2976 (imp
20	pir2.C83022	+	107.50	147.76	0.4562	998	!	probable two-component sens
21	pir2.1845554	+	107.00	154.26	0.5124	748	!	PEARL 4 protein [imported]
22	pir2.C683372	+	107.00	153.03	0.5218	377	!	heat shock protein B - Heli
23	pir2.150620	-	106.50	142.25	0.6680	1173	!	hypothetical protein PA281
24	pir2.142730	+	105.00	129.26	1.05	3942	!	prockr2 - chicken (fragmen
25	pir2.A81318	+	104.50	151.34	0.8284	295	!	Bassoon protein - mouse
26	pir2.180951	+	104.50	146.55	0.8895	509	!	probable Lipid A biosynthes
27	pir2.130251	+	104.50	139.50	0.9872	1130	!	zinc finger protein Ckr1 -
28	pir2.836149	+	104.50	137.00	1.02	1500	!	repetin - mouse
29	pir2.1448818	+	104.50	134.37	1.07	2022	!	copper-transferring AtPase
30	pir2.S27953	+	104.00	151.45	0.9026	267	!	glucan 1,4-alpha-glucosida
31	pir2.1887520	+	103.50	147.37	0.9588	424	!	Mx protein - pig (fragment
32	pir2.1931421	+	103.00	137.63	1.21	1173	!	hypothetical protein CC2193
33	pir2.1887000	+	103.00	147.22	1.14	362	!	C-terminal domain-binding
34	pir2.AE1071	+	102.50	145.04	1.129	425	!	hypothetical protein CC2597
35	pir2.A56360	+	102.00	140.02	1.52	425	!	Dmx protein [imported] - S
36	pir2.166118	+	101.50	134.62	1.51	688	!	zinc finger protein (clone
37	pir1.EB6116	+	101.50	132.62	1.85	312	!	hypothetical protein (sdsb
38	pir2.E97631	+	101.00	141.73	1.76	1460	!	immediate-early protein IE
39	pir2.E07339	+	100.50	143.91	1.86	476	!	probable membrane transport
40	pir2.A69046	+	100.50	139.15	2.00	584	!	plastoquinol1-plastoquin
41	pir2.T30136	+	100.50	138.19	2.03	654	!	conserved hypothetical prot
42	pir2.10C5580	+	100.50	127.44	2.38	2206	!	hypothetical protein C14C11
43	pir2.118182	+	99.50	130.70	2.70	1279	!	voltage-dependent calcium
44	pir2.T131422	+	99.50	129.46	2.75	1473	!	hypothetical protein L7610
45	pir2.T333997	+	99.00	138.74	2.61	471	!	C-terminal domain-binding
46	pir2.B75310	+	99.00	137.73	2.65	528	!	hypothetical protein W0361
47	pir2.C54152	+	98.00	143.55	2.90	228	!	conserved hypothetical prot

A:Accession: D81986
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <PKR>
A:Cross-references: GB:AL162753; GB:AL157959; MID:g7379120; PIDN:CAB83949.1; PID:g737939
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0662

alignment_scores:
Quality: 1580.00 Length: 298
Ratio: 5.302 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-303-518D-569 x D81986 ..

Align seg 1/1 to: D81986 from: 1 to: 298

```
1 ATGTTTGGTTTACATTCAGGCTGTTCCCTTGGACCCGATGCA 50
|||||
1 MetPheArgLeuGlnPheArgLeuPheProPheLeuArgThrAlaMetHis 17
51 CATCCGTGTGACCGCCCTGCTCAAAATGCTCTCCCTGCTGCGCTTCT 100
|||||
17 sileleuLeuThrAlaLeuLeuLysCysLeuSerLeuLeuProLeuSerc 34
101 GTCTGCACACGCTGGGAAACCGGCTCGACATCTGGCGTTTACCTTTA 150
|||||
34 yslEuhisthrLeuGlnAsnArgLeuGlnHisLeuAlaPheArgLeuLeu 50
151 AAGGAAGACCGGCGGCGATGCTGCCAATATGCTGACGCGGATGAA 200
|||||
51 LysGlnAspArgAlaArgIleValAlaAsnMetArgGlnAlaGlyMetAs 67
51 nProAspProLysThrValLysAlaValPheAlaGlnThrAlaLysGly 84
251 GTTTGGAACTTGGCCCCGCTTTTTCAGAAAACCGGAAGACATAGAAACA 300
|||||
84 LysGlnLeuAlaPheAlaPheArgLysProGlnAspIleGlnThr 100
301 AAGTTCAAGCGGTACAGCGCTGGGAACTGTGCAGACGCTTGGCAAA 350
|||||
101 MetPheLysAlaValHisGlyThrGlnHisValGlnGlnAlaLeuAspLys 117
351 ACACGAAGGGCTGTATTCATCAGCCCGCACATGCGGACATAGATTGG 400
|||||
117 shisGlnGlyLeuLeuPheIleThrProHisIleGlySerTyrAspLeuG 134
401 GGGGACGCTACATCAGCCGACGCTTCCGCTGCGTACGCGCATGAC 450
|||||
134 LysGlnArgTyrIleSerGlnGlnLeuProPheProLeuThrAlaMetLys 150
451 AAACGCGCCAAATCAAGCGATAGCAAAATCATGACAGCGGCGAGGTT 500
|||||
151 LysProProLysIleLysAlaIleAspLysIleMetGlnAlaGlyArgVal 167
501 TCGCGGCAAGGAAACCGCGCTTACGACATACAGGGGTCAACAA 550
|||||
167 LArgGlyLysGlyLysThrAlaProThrSerIleGlnGlyValLysGlnI 184
551 TCATCAAGCGCTGCTGTTGGGCGGAAACATGCTGCTGCGCGACAC 600
|||||
184 IeLleLysAlaLeuArgSerGlyGlnAlaThrIleValLeuProAspHis 200
601 GTCCCTCCCTCAAGAAAGCGGCGGAAAGCGATGAGGTGATTTCTTCG 650
|||||
201 ValProSerProGlnGlnGlyGlyGlnGlyValLysPheValAspPheMet 217
651 CAAACCTGCTTATACCATGACGCTGGCGGCAAAATTTGGCACACGTC 700
```

seq_name: plr2:B81040

seq_documentation_block:

HTB/MSDB family protein NMB1801 [imported] - Neisseria meningitidis (strain MC58 ser C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: B81040
R:Retlein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MUID:20175755
A:Accession: B81040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <PEP>
A:Cross-references: GB:AE002530; GB:AE002098; MID:g7227054; PIDN:AAF42138.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1801

alignment_scores:
Quality: 1577.00 Length: 298
Ratio: 5.292 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.664

alignment_block:
US-09-303-518D-569 x B81040 ..

Align seg 1/1 to: B81040 from: 1 to: 298

```
1 ATGTTTGGTTTACATTCAGGCTGTTCCCTTGGACCCGATGCA 50
|||||
1 MetPheArgLeuGlnPheArgLeuPheProPheLeuArgThrAlaMetHis 17
51 CATCCGTGTGACCGCCCTGCTCAAAATGCTCTCCCTGCTGCGCTTCT 100
|||||
17 sileleuLeuThrAlaLeuLeuLysCysLeuSerLeuLeuProLeuSerc 34
101 GTCTGCACACGCTGGGAAACCGGCTCGACATCTGGCGTTTACCTTTA 150
|||||
34 yslEuhisthrLeuGlnAsnArgLeuGlnHisLeuAlaPheArgLeuLeu 50
151 AAGGAAGACCGGCGGCGATGCTGCCAATATGCTGACGCGGATGAA 200
|||||
51 LysGlnAspArgAlaArgIleValAlaAsnMetArgGlnAlaGlyMetAs 67
67 nProAspProLysThrValLysAlaValPheAlaGlnThrAlaLysGly 84
```

```

251 GTTGGAACTTGCCCGCGCTTTTCAGAAAACCGGAACATAGAAAC 300
    |||||||
84  LyeuGIleuAlaProAlaPhePheArgIysProGluAspIleGluThr 100
    |||||||
301 ATGTTCAAACCGGTACACGGCTGGGAACATGTCACAGCGTTTGACAA 350
    |||||||
101 MePheYsaIaValaHisGlyTrpGluHisValGlnGlnAlaLeuAspY 117
    |||||||
351 ACAGAAAGGCGCTGTATTCATCAGCGCGACATCGGCACCTTCGATTGG 400
    |||||||
117 SHISGluGlyLeuLeuPheHeliethrProHisIleGlySerTyrAspLeuG 134
    |||||||
401 GCGGACGCTACATACACGACGCTTCGCTCCGCTGACCGGCATGTAC 450
    |||||||
134 YglYArgTyrIleSerGlnGlnLeuProPheProLeuThrIleMetTyr 150
    |||||||
451 AAACCGCGGAAATCAAGCGATAGCAAAATCATCAGCGCGGACGGGT 500
    |||||||
151 LysProProLysIleLeuYsaIaIleAspYsIleMetGlnAlaGlyArgVa 167
    |||||||
501 TCGCGGCAAGGAAAGAAACCGCGCTACACGATACAGAGGCTCAACAA 550
    |||||||
167 LArgGlySglYsThrAlaProThrSerIleGlnGlyValYsGlnI 184
    |||||||
551 TCATCAAAAGCGCGCTGGGCGGGAAGCAACCATGCTCCTGCCGACAC 600
    |||||||
184 IeIleYsaIaLeuArgSerGlyGlnAlaThrIleValaLeuProAspHis 200
    |||||||
601 GTCCCGCTCCCTCAAGAAAGCGGGAAGCGCTATGGTGGATTTCCTGG 650
    |||||||
201 ValProSerProGlnGlnGlyGlyGlnGlyValITrPvalAspPhePheG 217
    |||||||
651 CAACCTGCGCTATACATGACGCTGCGGCAAAATGTCGACACGTCAAAG 700
    |||||||
217 YysProAlaTyrThrMetThrLeuAlaIaIaYsLeuAlaHisValYsG 234
    |||||||
701 GCGTAAACCGCTGTTTTCGTCGCAAGCGCTGCGGCGGCAACAGT 750
    |||||||
234 YValIysThrIleuPhePhePheCysGlyAlaGlyLeuProGlyGlnI 250
    |||||||
751 TTCGATTGTCACATCCGCCCGCTCCAAAGGGAATGAACGGCGACAAAGC 800
    |||||||
251 PheAspLeuHisIleArgProValGlnGlyIleuLeuAsnGlyAspYsaI 267
    |||||||
801 CCATGATGCGCGCGCTTCACACCGCAATGCCGAATATGATAGCGCGT 850
    |||||||
267 AhisAspAlaIaValaPheAsnArgAsnAlaGlnTyrTrpIleArgArgP 284
    |||||||
851 TTCGACGCGAGTATCTGTTATGTACACCGCTACAAATATGCGC 894
    |||||||
284 heProThrGlnTyrLeuPheMetTyrAsnArgTyrLysMetPro 298
    |||||||
seq_name: p1r2:C82691

seq_documentation_block:
  Lipid A biosynthesis lauroyl acyltransferase XF1348 [imported] - Xylella fastidiosa (str
  C/Species: Xylella fastidiosa
  C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
  C/Accession: C82691
  R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
  Nature 406, 151-157, 2000
  A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
  A:Reference number: A82515; NUID:20365717
  A:Note: for a complete list of authors see reference number A59328 below
  A:Accession: C82691
  A:Status: preliminary
  A:Molecule type: DNA
  A:Residues: 1-316 <SIM>
  A:Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84157.1; GSPDB:GN001
  A:Experimental source: strain 9a5c
  R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; A
  Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, F
  as Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.J.S.

```

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mitaca, E.C.; Miyaki, C.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1348

alignment_scores:
Quality: 263.50 Length: 286
Ratio: 1.532 Gaps: 9
Percent Similarity: 60.140 Percent Identity: 27.273

alignment_block:
US-09-303-518D-569 x C82691 ..

Align seg 1/1 to: C82691 from: 1 to: 316

```

103 CTGCACACGCTGGGAACCGGCTCGACATCTGGCTTTACCTTTAA 152
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
10  LeuYTrArgValAlaSerLeuValGlyHisIleProThrProPheLeu 26
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
153 GGAAGACCGCGCGCATCGCGCC.....AATATGC 184
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
26  sArg...LeuSerAspLeuIleAlaTyrCysTrpLeuCysLeuAsnAla 42
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
185 GTGACGGA.....GGCATG 198
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
42  rGlnSerArgValThrGlnArgAsnLeuGluLeuThrTyrProGluLeu 58
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
199 AATCCGACCCCAAAAGC.....GTCAAGCGCTTTGCGGAACGCG 242
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
59  SerProGlnGlnHisThrArgLeuHisHisGlnIleIleTyrSerThrVa 75
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
243 AAAAGCGGTTTGGAACTGCGCGCGGCTTTTCAGAAAACCGGAAGCA 292
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
75  LArgGlnAlaPheGluMetLeuHisIleTrpThrHisProGluThrGln 92
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
293 TAGAAACATGTTCAAAGCGGTACACGCGTGGGAACATGTGCGACGCT 342
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
92  snLeuAlaArgLeuArgGluTyrHisGlyValaAspLeuTyrSerAlaAla 108
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
343 TTGGACAAACGACGAAGGCGTGTATTCATCAGCGCGCACATCGGACGTA 392
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
109  LeuAlaArgAsnArgGlyMetIleIleValaProHisPheLeuYsnTr 125
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
393 CGATTGGCGGCGACGCTACATCAGCGACGAGCTCGGTCGCGTACGCG 442
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
125  pGluLeuLeuYsGlnTyrLeuSerAspLeuAla.....ProLeuThrL 140
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
443 CCATGTACAAACCGCGCAAAATCAAGCGATGACAAATTCATCGAGCGG 492
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
140  euMetTyrArgProAlaAsnSerAlaValaLeuAspGlyPheLeuGln 155
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
493 GCGAGGCTTCGCGCAAGGAAACCGCGCTACAGCATCAAGAGG... 540
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
156  ...ArgValaArgGlyGlyAsnAsnValaHisGlnValaArgAlaGlnGly 171
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
541  ...GTCAAACAATCATCAAGCGCTGCGGTCGCGGCGACGACCATCG 586
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
171  laValaArgHisLeuPheHisValaLeuYsaGlnGlyTrpIleGlyI 188
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
587  TCTGCGCGGACGACGTCCTCCCTCAAGAGGCGGGAAGCGCTATAG 636
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
188  leuLeuProAspGlnGlnPro.....LysIleGlyGlyGlnValaPhe 201
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```


A:Cross-references: GB:AE004747; GB:AE004091; NID:99949362; PIDN:AA06630.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: SA3242

alignment_scores:
 Quality: 228.50 Length: 281
 Ratio: 1.336 Gaps: 6
 Percent Similarity: 60.854 Percent Identity: 26.335

alignment_block:
 US-09-303-518D-569 x D83239 ..

Align seg 1/1 to: D83239 from: 1 to: 312

```

67 CTGCTCAATGCTCTCCCTGCTGCGCTTTCTGTCACACGCTGG 116
|||||  :: |||||  |||
24 LeuLeuTrpLeuValValGlnLeuProTyrProValLeuLeuMetLeuG1 40
117 AACCGGCTCGACATCTGGCTTTTACTTTTAAAGGAAGACCGCGC 166
|||  |||||  |||  |||  :: |||
40 YtrgGlyLeuGlyAlaLeuMetTyrArgLeuValGlySerArgTyrGluI 57
167 GCATGCTGCCAATATGCTCAGCGAGCATGATCCGACCC... 210
:: |||||  :: |||
57 LeuAlaIArgAsnLeuGlnLeuGlyPheProGlnLysSerProAlaGlu 73
211 .....AAACGGTCAAAACCGTTTGGGAAACGGCAAAAGCGGTTT 254
:: |||||  |||||  :: |||
74 ArgGluArgLeuLeuLysGlnAsnPheAlaSerGlyIleAlaPhePh 90
255 GGACTTGGCCCGCGTTTTCAGAAACCGGAAGACATAGAACATCT 304
|||||  :: |||||  |||||  :: |||
90 eGlnMetAlaMetSerTyrTrp...TyrProLysAlaArgLeuAlaArgL 106
305 TCAAACGGGACACGCTGGGAAACATGTCAGAGGCTTGGCAAAAC 354
:: |||||  |||||  :: |||
106 euaLHisIleGlnGlyLeuGlnHisLeuArgGlnAlaGlnAlaGlnGly 122
355 GAAGGCTGCTATTTCATCAGCGGCACATCGGAGCTACGATTGGCGG 404
|||||  :: |||||  :: |||||  :: |||
123 GlnGlyValIleLeuMetAlaLeuHisPheThrThrLeuGlnIleGlyAl 139
405 AGCGTACATCAGCCAGACGCTCCGCTCCGCTGACCGCCATGTACAA 454
:: |||||  :: |||||  :: |||
139 AlaLeuLeuGlnGlyGln...ValHisThrIleAspGlyMetTyrArg 154
455 CGCGGAAATTCAAAGGATAGCAAAATCATGCGCGGAGGCTTGGC 504
|||||  :: |||||  :: |||
154 IuHisAspAsnProValPheAspTyrValGlnArgArgGlnArgGluArg 170
505 GGCAGAGGAAAGAAACCGCGCTACACATACAGAGGGGTCAAAACAT 554
:: |||||  :: |||||  :: |||||  :: |||
171 HisAsnLeuAspAlaThrAlaIleGlnArgGlnAspValArgSerMetLe 187
555 CAAAGCCCTGCGTTGGGCGAGCAACCATGCTGCGCGCGACACAGTCC 604
:: |||||  :: |||||  :: |||||  :: |||
187 uLysValLeuArgGlyGlyArgAlaIleTyrTyrAlaProAsp..... 201
605 CCGCCCTCAAGAGGCGG...GAAGCGGTATGGGATTTCTTC 648
|||||  |||||  :: |||||  :: |||||  :: |||
202 .....GlnAspTyrGlyAlaLysGlnSerLeuPheValProLeuPhe 215
649 GGCAGAACCTGCTTATCAGATGAGCTGGCGCAAAATGGACACGTC 698
|||  |||||  |||||  :: |||||  :: |||||  :: |||
216 GlyIleProAlaThrValThrAlaThrThrLysPheAlaArgLeuG1 232
699 AGCGGTGAAACCCGTTTCTGCTGCGAGACCGCTGCGCGACAG 748
:: |||||  :: |||||  :: |||||  :: |||
232 YArgAlaArgValLeuProPheThrGlnSerArgLeuAlaAspGlySer 249
749 GTTTCGATTTCGACATCCGCCGCTCAAGGGAATTGAACGGCGACAAA 798

```

```

|||||  |||  |||||  :: |||||  :: |||||  :: |||||  :: |||||
249 IyTyrArgLeuThrIleHisProProLeuLysPheProGlnGlyLys 265
799 GCCCAT...GATGCCCGCGTGTTCACCGCAATGCGGATATTGGATAG 845
:: |||||  :: |||||  :: |||||  :: |||||  :: |||||
266 GlnGlnAlaAspCysLeuArgIleAsnGlnTrpValGlnArgCysValAla 282
846 CCGTTTCCGACGATGCTGTATGTACACCGCTACAAA 888
|||||  |||  |||||  :: |||||  :: |||||  :: |||||
282 gGlnGlnProGlnGlnIleuTrpAlaHisArgArgPheLys 296
seq_name: pir2:SI6888

```

```

seq_documentation_block:
lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) - Escherichia coli
N:Alternate names: htrb protein
C:Species: Escherichia coli
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: SI6888; A42290; C64848
R:Karow, M.; Georgopoulos, C.
Mol. Microbiol. 5, 2285-2292, 1991
A:Title: Sequencing, mutational analysis, and transcriptional regulation of the Esche
A:Reference number: SI6888; M01D:92114808
A:Accession: SI6888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <KAR>
A:Cross-references: EMBL:X61000; NID:948950; PIDN:CAA43317.1; PID:948957
A:Experimental source: strain K-12
R:Ueguchi, C.; Ito, K.
J. Bacteriol. 174, 1454-1461, 1992
A:Title: Multicopy suppression: an approach to understanding intracellular function in
A:Reference number: A42290; M01D:92165719
A:Accession: A42290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 200-306 <UEG>
A:Cross-references: EMBL:X59939; NID:942028
A:Experimental source: strain K-12
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; M01D:97426617
A:Accession: C64848
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-306 <BLAT>
A:Cross-references: GB:AE000206; GB:U00096; NID:91787282; PIDN:AC74138.1; PID:917872
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: htrb
C:Function:
A:Description: acylates the intermediate (Rdo)2-1-lipid IVA
A:Pathway: lipopolysaccharide biosynthesis
A>Note: required for bacterial viability above 33 degrees C in rich media
C:Keywords: acyltransferase; lipopolysaccharide biosynthesis; transmembrane protein
F:21-37/Domain: transmembrane #status predicted <TMM>

```

alignment_scores:
 Quality: 215.00 Length: 274
 Ratio: 1.303 Gaps: 9
 Percent Similarity: 60.219 Percent Identity: 29.197

alignment_block:
 US-09-303-518D-569 x SI6888 ..

Align seg 1/1 to: SI6888 from: 1 to: 306

```

88 CTGCGGCTTTCCTGTCACACGCTGGGAAACCGCTCGACATCTGCG 137
|||||  :: |||||  |||||  :: |||||  :: |||||
32 LeuProTyrProValIleTyrArgLeuGlnCysGlyLeuGlyLysLeuAl 48

```


Percent Similarity: 57.092 Percent Identity: 29.078

alignment_block:
US-09-303-518D-569 x A10441 ..

Align seg 1/1 to: A10441 from: 1 to: 306

```

67 CTGCTCAAAATGCTCTCCCTGCTGCGCTTCTCTGTGCACACGCTGG 116
   :::::  |||  |||||  |||||  |||||
25 VALLEupheLeuValGlnLeuProtyrProLeuLeuAsnLysLeuG1 41
   :::::  |||  |||||  |||||  |||||
117 AACCGGCTCGACATCTGGCGCTTTTACCTTTAAAGAAAGCGCGCGC 166
   |||||  :::::  :::::  :::::  |||
41 yAltrLeuGlyArgInSerMetArgPheLeuLys.....ArgArgV 56
167 GCATGGTGGCAATATGGCTCAGGACGATGAATCCGAC..... 207
56 aISerLeuAlaArgAsnLeuGlnLeuCysPheProAspMetAspLys 72
208 .....CCCAAAACGGTCAAAACCGCTTTTGGGAAACGGCAAAAG 248
73 GlnValLeuGlnGlnThrLeuLeuGlnPheGlnSerLeuGlnMetG1 89
249 CGGTTTGGACCTTGGCCCCGCTTTTTCAGAAACCGCAACATAGAAA 298
   |  |||||  :::::  |||||  :::::  |||||
89 yLeuLeuGlnThrGlyMetAlaTrpPheTrpSerAspThrArgLysGln 106
299 CAATGTTCAAGCGGTACACGCGTGGGAACATGTCACAGCGCTTTGGAC 348
106 rGTTrpPhe...SerValSerGlyLeuGlnAsnLeuLysArgAlaGlnGln 121
349 AAACAGCAAGGGCTGCTATTCATCAAGCGCGCACATGCGACGCTACGAT 398
   :::::  |||  |||||  |||||  |||||
122 GlyLysArgGlyValLeuValIleGlyValHisPheMetSerLeuGln 138
399 GGGCGGACGCTACATCAGCAGCAGCTTCCGCTCCGCTGACCGGCAGT 448
138 uGlyGlyArgValMetGlyGlnCysGln.....ProMetLeuAlaMet 153
449 ACAAAACCGCGCAAAATCAAAAGCATAGCAAAATCATGACGGCGGCGAG 498
   :::::  |||  |||||  |||||  |||||
153 yArgProHisAsnAsnLysValMetGlnLeuValGlnThrTrpLysArg 169
499 GTTCGGCGCAAGAAAGAAACCGCGCTACACGATACAAAGGGGTCAAAA 548
   :::::  |||  :::::  :::::  :::::
170 MetArg.....SerAsnLysAlaMetLeuAspArgAlaGlnLysG1 184
549 AATCATCAAGGCGCTGCTGCGGGAAGCAACCATCGCTCGCCGCGAC 598
184 yMetValArgAlaLeuLysGlnGlyGlnAlaValTrpPheAlaProAspG 201
599 ACGTCCCTCCCTCCCAAGAAAGCGGGGAAGCGATGAGTGGATTTCTTC 648
   :::::  |||||  :::::  :::::  :::::
201 InAspTrpLysProArg.....GlySerValPheAlaLeuPhe 214
649 GGC...AAACSTGCTATACATGACGCTGCGGCAAAATGGCACAGCT 695
   :::::  |||  |||||  :::::  :::::
215 AlaValGlnHisAlaLeuThrThrSerGlyThrPheMetLeuAlaArg 231
696 CAAGGCGTGAAGAACCGCTTTTCTGCTGCGAAGCGCGCTGCGCGAC 745
231 uAlaLysProAlaLeuLeuProLeuValLeuLeuTrpLysLysGlnGly 248
746 AAGTTTCATTTGCACATCGCCGCTCCCAAGGGAATTGAAC...GGC 792
   :::::  |||||  |||||  |||||  :::::
248 rGgLyLysPheLeuLeuLeuGlnProAlaLeuGlnAspTrpProLysP 264
793 GACAAAGCCCATGATCGCGCTGTTCACACCGCAATGCCGAATATGGAT 842
   |||||  :::::  :::::  :::::  |||
265 AspGlnIleAlaIleAlaSerTrpMetAsnLysValIleGlnLysGln 281
843 ACGCGTTTTCGACGACGATCTGTATGTATGACAAACGCTACAA 888
   |  |||  |||  |||||  :::::  :::::  :::::

```

281 emetArgAlaProGlnLysLeuThrLeuPheLeuHisArgArgPheLys 296
seq_name: p1r2:D81085

seq_documentation_block:
HitB/MSDB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 ser C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
R:Accession: D81085
C:Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755
A:Accession: D81085
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <TEXT>
A:Cross-references: GB:AE002491; GB:AE002098; NID:g7226655; PIDN:AAF41779.1; PID:g722 A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1418

alignment_scores:
Quality: 204.50 Length: 286
Ratio: 1.225 Gaps: 11

Percent Similarity: 58.392 Percent Identity: 26.923

alignment_block:
US-09-303-518D-569 x D81085 ..

Align seg 1/1 to: D81085 from: 1 to: 289

```

67 CTGCTCAAAATGCTCTCCCTGCTGCGCTTCTCTGTGCACACGCTGG 116
   :::::  |||||  :::::  |||||  :::::
7 ValLeuTrValLeuGlnPheLeuProPheAlaLeuLeuHisLysLysIleAl 23
117 AAACCGGCTCGACATCTGCGCTTTTACCTTTAAAGAAAGCGCGCGC 166
   :::::  |||  |||||  |||||  |||
23 aAspLeuThrGlyLeuLeuAla...TyrLeuLeuValLysProArgArg 39
167 GCATC.....GTGCCAATATGCTGACGCGACGATGATCC 204
   |||||  :::::  :::::  :::::  :::::
39 rGlyGlyGlnIleAsnLeuAlaLysCysPheSerGlnTrpSerGlnGln 55
205 GACCCCAAAACGTC...AAAGCGTTTTCGCGAAACGGCAAAAGCGG 251
   |||||  |||||  |||  :::::  |||||
56 LysArgLysThrValLeuLysGlnHisPheLysHisMetAlaLysLeu 72
252 TTGGAAGCTTGGCCCGCTTTTTCAGAAACCGAAGCATAGAAACA 301
   |||||  :::::  :::::  :::::  :::::
72 tLeuGlnTyrGlyLeuLysTrpTrpTrpArgProAlaGlyArgLeuSer 89
302 TGTTCAAAGCGGTACACGCGTGGGAACATGTCACAGGCTTTGCAACA 351
   :::::  :::::  :::::  :::::  |||||
89 euValArg...TyrArgAsnLysHisTyrLeuAspAspAlaLeuAla 104
352 CACGAAGGCTGCTATTCATCAGCGCGCACATGCGGACGATGATTTGG 401
   |||  :::::  :::::  |||||  :::::
105 GlyLysValIleIleLeuLysGlnHisPheThrAlaPheGlnMetAl 121
402 CGAGCGTACATCAGCCAGCAGCTCCGCTTCCGCTGACCGCATGTACA 451
   :  :::::  |||||  :::::  |||||
121 aValTyrAlaLeuAsnGlnAspLys.....ProLeuIleSerMetLys 136
452 AACCGCGAAATCAAGCGATGACAAATCATGACGCGGCGAGGTT 501
   ::  |||  :::::  :::::  :::::
136 eHisGlnLysAsnLysIleLeuAspGlnLysLeuLysGlyArgAsn 152
502 CGCGCAAGGAAGAAACCGCGCTACACGATACAAAGGGTCAAAAT 551

```



```

153 ArgTyrHisAsnValPheLeuIleGlyArgThrGlyLeuArgAlaIle 169
552 CATCAAGACCCCTGCGTTCGGCGCAAGCAAC...ATCGCTCGCCGACG 598
169 uValLysGlnPheArgLysSerSerAlaProPheLeuTyrLeuProAsp 185
599 ACGTCCCTCCCTCAAGAGCGGG...GAAGGGCTATGGGTGAT 642
186 .....GlnAspPheGlyArgAsnAspSerValPheValAsp 197
643 TTCTTGGCAACCTGCTATACCATGACGCGCGCAAAATTTGACACA 692
198 PhePheGlyIleGlnThrAlaThrIleThrGlyLeuSerArgIleAlaAl 214
693 CGTCAAGCGCTGAAGAACCCCTTTTTCGTCGCAAGCCCTGCT... 738
214 aLeuAlaAsnAlaLysValIle.....ProAlaIleProValA 227
739 .....GGCGGACAGGTTTCGATTTCACATCCGCCCGCTCCAGGGGA 783
227 rGgluAlaAspAsnThrValThrLeuHisPheTyrProAlaIrrLysSer 243
784 TTGAACGGCGACAAAGCCCAT...GATGCCGCGCTTCAACCGCAATGC 830
244 PheProGlyGluAspAlaLysAlaAspAlaGlnArgMetAsnArgPheI 260
831 CGAATATTGATACGCGCTTTCGACGACCATCTGTTATGTCACAC 880
260 eGluAspArgValAlrGlnHisProGlnGlnTyrPheThrLeuHisLysA 277
881 GCTACAA 888
277 rGphelys 279

seq_name: pir2:B81857

seq_documentation_block:
probable acetyltransferase NMA1630 [imported] - Neisseria meningitidis (strain Z2491 ser
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; M0ID:20222556
A:Accession: B81857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CA84858.1; PID:9738027
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1630

alignment_scores:
Quality: 203.50 Length: 285
Ratio: 1.219 Gaps: 9
Percent Similarity: 58.596 Percent Identity: 25.965

alignment_block:
US-09-303-518D-569 x B81857 ..

Align seg 1/1 to: B81857 from: 1 to: 289

```

```

23 aAspLeuThrGlyLeuLeuAlaTyrLeuLeuValLysProAlrArgArgI 40
167 GCATCTGCGCCCAATATGCGTCGACGAGCATGATCCCGCAAAAG 216
40 leGlyGlnIleAsnLeuAlaLysCysPheProGluTrrPaspGlyLys 56
217 GTCAAGCCGTT.....TTTGGGAAAGCGCAAAAGCGGTTT 254
57 ArgLysThrValLeuLysGlnHisPheLysHisMetAlaLysLeuMet 73
255 GGAACCTGGCCCCCGTTTTCAGAAAACCGAAGACATGAAACAATGT 304
73 uGlnTyrGlyLeuTyrTrrPrrAlaProAlaGlyArgLeuLysSerLeu 90
305 TCAAGCGGTACAGCGCTGGACATGTGACAGGCTTGGCAAAAC 354
90 alArg...TyrArgAsnLysHisTyrLeuAspAspAlaLeuAlaGly 105
355 GAAGGCTGCTATTATCATCAGCGCGACATCGCACTAGCATTTGGGCG 404
106 GlnLysValIleIleLeuTyrProHisPheThrAlaPheGlnMetAla 122
405 ACGCTACATCAGCGACGCTTCGCTCCGCTGACCGCATGACAAAC 454
122 lTrrAlaLeuAsnGlnAspVal.....ProLeuIleSerMetLysSer 137
455 CGCCGAAATCAAGCGATAGACAAATCATGACAGCGGCGAGGTTTCG 504
137 lsglnLysAsnLysIleLeuAspGlnGlnIleLeuLysGlyArgAsnArg 153
505 GCGAAAGGAAAACCGCGCTACCAGCATCAAGGGGTCAACAAATCAT 554
154 TyrHisAsnValPheLeuIleGlyArgThrGlnGlyLeuArgAlaLeu 170
555 CAAAGCCCTGCGTTTCGGCGCAAGCAAC...ATCGCTCGCCGACGAC 601
170 lLysGlnPheArgLysSerSerAlaProPheLeuTyrLeuProAsp... 185
602 TCCCTCCCTCAAGAGCGGG.....GAAGCCTATGGGTGATTC 645
186 .....GlnAspPheGlyArgAsnAspSerValPheValAspPhe 198
646 TTGCGCAAACTGCTATACCATGACGCTGCGCGCAAAATTTGACACGT 695
199 PheGlyIleArgThrAlaThrIleThrGlyLeuSerArgIleAlaIle 215
696 CAAGGCGGTGAAGAACCCCTGTTTTCGTCGCAAGCCCTGCT... 738
215 uAlaAsnAlaLysValIle.....ProAlaIleProValArg 228
739 ..GGCGGACAGGTTTCGATTTCACATCCGCCCGCTCCAGGGGAATG 786
228 lAlaAspAsnThrValThrLeuHisPheTyrProAlaIrrLysSer 244
787 AACGGCGACAAAGCCCAT...GATGCCGCGCTTCAACCGCAATGCCA 833
245 ProSerGluAspAlaGlnAlaAspAlaGlnArgMetAsnArgPheIle 261
834 ATATTGGATACGCGCTTTCGACGACGATGCTGTTATGTCACACCGT 883
261 uGlnArgValAlrGlnHisProGlnGlnTyrPheThrLeuHisLysArg 278
884 ACADA 888
278 helys 279

seq_name: pir2:AD0807

seq_documentation_block:
probable acyltransferase (EC 2.3.1.-) [imported] - Salmonella enterica subsp. enteric
C:Species: Salmonella enterica subsp. enterica serovar typh
A>Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

```



```

215 LuAlaValTrpPheAlaProAsp.....GlnsPtyrGly 226
625 GAA.....GGCGTATGGGTGATTTCTTTCGGC...AAACCTGCTATAC 665
::: :::: ::::: ::::: ::::: ::::: ::::: :::::
227 ArgLysIlySerSerPheAlaProPheAlaValGlnsValAlaThr 243
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C/Accession: G65011
R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G65011
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <BLAT>
A:Cross-references: GB:AE000326; GB:U00096; NID:q1788718; PIDN:AACT5437.1; PID:q1788721;
A:Experimental source: strain K-12, substrain MG1655
C:Keywords: acyltransferase; lipopolysaccharide biosynthesis; transmembrane protein
F:20-40/Domain: transmembrane #status predicted <TM2>
F:125-145/Domain: transmembrane #status predicted <TM2>

```

```

seq_name: p1r2:G65011
seq_documentation_block:
probable lauroyl acyltransferase b2378 - Escherichia coli
N:Alternate names: probable lipid A biosynthesis, protein b2378
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C/Accession: G65011
R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G65011
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <BLAT>
A:Cross-references: GB:AE000326; GB:U00096; NID:q1788718; PIDN:AACT5437.1; PID:q1788721;
A:Experimental source: strain K-12, substrain MG1655
C:Keywords: acyltransferase; lipopolysaccharide biosynthesis; transmembrane protein
F:20-40/Domain: transmembrane #status predicted <TM2>
F:125-145/Domain: transmembrane #status predicted <TM2>

```

```

alignment_scores:
Quality: 189.50 Length: 294
Ratio: 1.199 Gaps: 12
Percent Similarity: 53.741 Percent Identity: 26.190

```

```

alignment_block:
us-09-303-518d-569 x G65011 ..

```

```

Align seg 1/1 to: G65011 from: 1 to: 328

```

```

88 CTGCGCGTTTCTGCTGCGACACGCTGGGAAACGGCTCGGACATCTGGC 137
||||| ||| ||||| ::::: ::::: ::::: :::::
54 LeuProTyPProValLeuLysPheLeuGlyThrArgIleGlyAlaMetAl 70
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: D85880
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoukis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: D85880
A:Status: preliminary

```

```

104 AsnPheArgSerLeuGlyMet..... 110
||||| ::::: ::::: ::::: :::::
228 TTTTGGGAAACGGCAAGCGGTTTGACACTTGCCCGCGCTTTTCA 277
::: ::::: ::::: ::::: :::::
111 .....AlaLeuValGluThrGlyMetAlaThrPheT 121
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: D85880
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoukis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: D85880
A:Status: preliminary

```

```

seq_name: p1r2:D85880

```

```

seq_documentation_block:
probable heat shock protein ddd [imported] - Escherichia coli (strain O157:H7, substr
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: D85880
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoukis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: D85880
A:Status: preliminary

```

A: Molecule type: DNA
 A: Residues: 1-328 <STO>
 A: Cross-references: GB:AE005174; NID:912516752; PIDN:AA657504.1; GSPDB:GN00145; UWGP:236
 A: Experimental source: strain 0157:H7, substrain EDL933
 C: Genetics:
 A: Gene: ddg

alignment_scores:
 Quality: 189.50 Length: 294
 Ratio: 1.199 Gaps: 12
 Percent Similarity: 53.741 Percent Identity: 26.190

alignment_block:

US-09-303-518D-569 x D85880 ..

Align seg 1/1 to: D85880 from: 1 to: 328

```

88 CTGCGCGCTTCTGCTGCACACGCTGGGAAACGGGCTGCGACATCTGGC 137
   ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
54 LeuProTyrProValLeuLysPheLeuGlyThrArgIleGlyAlaMetAl 70
138 GTTTTACCTTTTAAAG..... 153
70 AArgProPheLeuLysArgArgIleAlaArgLysAsnLeuGlu 87
154 .....GAAGACCGCGCGCGCATCGTCGCC... 177
87 eucysPheProGlnHisSerAlaGlnIleValArgLysMetIleAlaGlu 103
178 AATATGCGCGACGAGCGATGAATCCGACCCCAAAACGGCTCAAAAGCCGT 227
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
104 AsnPheArgSerLeuGlyMet..... 110
228 TTTTCCGGAACGCGAAAGCGGCTTTGGAATTCGCCCGCTTTTCA 277
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
111 .....AlaLeuValGluThrGlyMetAlaIlePheT 121
278 GAAACCGGAGACATAGAACATGTTCAAAGCGGTACAGCGCTGGGAA 327
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 rPProAspSerArgValArgLysTrpPheAsp...ValGluGlyLeuAsp 136
328 CATGTGACGAGCGCTTTGGACAACACGAGGCGCTATTCATCAGCCGC 377
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 AsnLeuLysArgAlaGlnMetGlnAsnArgLysValMetValIleGlyVa 153
378 GCACATCCGCGACGTACATTTGGGCGGACGCTACATCAGCCAGCGCTTC 427
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
153 IHisPheMetSerLeuGlnIleGlyArgValMetGly.....Leuc 168
428 CGTTCCCGTCGACCGCCATGTACAAACCGCGAAATCAAAAGCATAGAC 477
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 ysgInPProMetMetAlaThrTyrArgProHisAsnAsnGlnLeuMetGlu 184
478 AAAATCATGACGCGCGGACGGGTTCG...GGCAAGGAAACCGCGGCC 524
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 TrpValGlnThrArgLysArgMetArgSerAsnLysAlaMetIleGlyAr 201
525 TACGACGATACAGGGGTCAAAATCATCAAAAGCCCTGCTGGCGCG 574
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 gAsnAsnLeuArgLys.....IleValGlyAlaLeuLysLysGly 215
575 AAGCAACCATGCTCTGCGCGACACGCTCCCTCCCTCAAGAGCGGG 624
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
215 IuAlaValTrpPheAlaProAsp.....GlnAspTyrGly 226
625 GAA.....GGCGTATGGTGATTTCTTCTGGC...AAACCTGCGTATAC 665
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
227 ArgLysGlySerSerPheAlaProPheAlaValGlnAsnValAlaThr 243
666 CATGACCGCTGCGCGCAAAATTTGCGACACGTCAAAAGCGGTGAAAAACCTGT 715
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
243 rThrAsnGlyThrTyrValLeuSerArgLeuSerGlyAlaAlaMetLeuT 260

```

```

716 TTTTCTGCTGGACAGCCCTGCTGGCGGACAGAGTTTGCATTCACATC 765
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
260 hrValThrMetValArgLysAlaAspTyrSerGlyTyrArgLeuPhe 276
766 CGCCCGCTCCAAAGGGAGATTCAGCGC.....GACAAAGCCCATGA 806
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
277 ThrPro.....GluMetGlnIleTyrProThrAspGlnAsnGlnAl 290
807 TGCCCGCGCTGTTCACACGCAATGCCGATATTCGATTCGCGCTTTCCG 856
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
290 alaAlaLysMetAsnLysIleIleGluLysGlnIleMetArgAlaProG 307
857 CGCAGTATCTGTTATGTACACCGCTACAAA 888
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
307 IuGlnTyrLeuThrIleHisArgArgPheLys 317

```

seq_name: p1r2:AD0637

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) (heat shock protein) [Impor
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: this species has also been called Salmonella typhi
 C:date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:accession: AD0637
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 , S.; Mout, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AD0637
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-306 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD08279.1; PID:916502326; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1192
 C:Keywords: acyltransferase

alignment_scores:
 Quality: 185.00 Length: 289
 Ratio: 1.194 Gaps: 8
 Percent Similarity: 53.633 Percent Identity: 24.221

alignment_block:

US-09-303-518D-569 x AD0637 ..

Align seg 1/1 to: AD0637 from: 1 to: 306

```

88 CTGCGCGCTTCTGCTGCACACGCTGGGAAACGGGCTGCGACATCTGGC 137
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
32 LeuProTyrProValLeuLysPheLeuGlyThrArgIleGlyAlaMetAl 48
138 GTTTTACCTTTTAAAG..... 153
48 AArgArgValMetLysArgArgAlaLysIleAlaLysTrpArgAsnLeuGlu 65
154 .....GAAGACCGCGCGCGCATCGTCGCC 177
65 eucysPheProGlnHisSerAlaGlnIleValArgHisThrMetValLys 81
178 AATATGCGCGACGAGCGATGAATCCGACCCCAAAACGGTCAAAAGCCGT 227
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
82 AsnPheGlnSerValGlyMet..... 88
228 TTTTCCGGAACGCGAAAGCGGCTTTGGAATTCGCCCGCTTTTCA 277
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 .....GlyValMetGlnThrGlyMetAlaIlePheT 99
278 GAAACCGGAGACATAGAACATGTTCAAAGCGGTACAGCGCTGGGAA 327

```

```

      ::::: ::::: ||| |||
99 rprpAspArgValAsnArgTrpMetGluAla...SerGlyLeuGlu 114
      ::::: ::::: ||| |||
328 CARGTGAGAGAGCGTTGGACAAACGAGAGCGGTGCTATTCATCAGCCG 377
      ::::: ::::: ||| |||
115 HisLleArgLValLysAlaGlnGlyLeuGlyPheLleLeuValGlyI 131
      ::::: ::::: ||| |||
378 GCACATCGGAGCTACGATTTGGCGGAGCGCTACATCAGCCAGCGCTTC 427
      ::::: ::::: ||| |||
131 eHisPheLeuThrLeuGlnPheGlyAlaArgMetPheGlyMetHisAsn 148
      ::::: ::::: ||| |||
428 CGTTCGCCGCTGACCGCCATGTACAAACCGCGGAAATCAAGGATPAG 477
      ::::: ::::: ||| |||
148 roGly.....LleGlyValTrpProAsnAspAsnProLeuLeuAsp 162
      ::::: ::::: ||| |||
478 AAATCATGCGGCGGAGGCTTCGCGGCAAGAAAGAAACCGCGCTAC 527
      ::::: ::::: ||| |||
163 TrpLeuGlnThrTrpGlyArgLeuArg.....SerAsnLysSerMetLe 177
      ::::: ::::: ||| |||
528 CAGCATACAGGGGTCAAAACATCATCAAAACCGCTTCGCGGCGAAG 577
      ::::: ::::: ||| |||
177 uAspArgLysAspLeuLysGlyMetValLysAlaLeuLysSerGlyI 194
      ::::: ::::: ||| |||
578 CAACCATGCTCTGCCGACCGACGCTCCCTCCCTCAAGAGCGGAGAA 627
      ::::: ::::: ||| |||
194 euLleTrpTrpAlaProAsnHisAspTrpGlyProArg.....Ala 207
      ::::: ::::: ||| |||
628 GCGCATGAGGTGATTTCTTCGCG...AAACCTCCCTATACCATAGAGCT 674
      ::::: ::::: ||| |||
208 SerValPheValProLeuPheAlaValAspGlnAlaAlaThrTrpSerG 224
      ::::: ::::: ||| |||
675 GCGCGCAAAATTTGGACACGTCGCAAGGCGTGAAACCGCTTTTTCGCT 724
      ::::: ::::: ||| |||
224 yThrTrpMetLeuAlaArgMetSerLysAlaCysLleLleProSerValP 241
      ::::: ::::: ||| |||
725 GCGAAGCGCTGCTGCGGACAGGTTTCGATTCGACATCCGCCCGCTC 774
      ::::: ::::: ||| |||
241 roArgArgLysProAspLysGlyTrpGluLeuLleLleProAla 257
      ::::: ::::: ||| |||
775 CAAGGGAATTCAGCGGAGCAAGCCGAT...GATGCCGCGCGTTTCA 821
      ::::: ::::: ||| |||
258 GlyTrpSerProProLeuGlnSerAlaGlnAlaThrAlaAlaTrpMetAs 274
      ::::: ::::: ||| |||
822 CCGCATATCGGCAATATTTGATAGCGCGTTTTCGAGCGAGATATCTGTTA 871
      ::::: ::::: ||| |||
274 nLysLleValGlnGlnIncysLleMetMetAlaProGlnGlnTrpMetTrpL 291
      ::::: ::::: ||| |||
872 TGTCACACCGCTACAAA 888
      ::::: ::::: ||| |||
291 euHisArgArgPheLys 296

```

seq_name: p1r2:164053

seq_documentation_block:

membrane-bound lytic transglycosylase homolog - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C/Accession: 164053

R/Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pline, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630

A/Accession: 164053

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-318 <TIGR>

A/Cross-references: GB:032705; GB:L42023; NID:g1573156; PIDN:AA21868.1; PID:g1573159; I

alignment_scores:

Quality: 178.50 Length: 275
Ratio: 1.137 Gaps: 9
Percent Similarity: 57.091 Percent Identity: 24.000

alignment_block:

US-09-303-518d-569 x 164053

Align seg 1/1 to: 164053 from: 1 to: 318

```

70 CTCAATGCGTCTCCCTGCTGCGGCTTCCTGTCGACACGCTGGGAAA 119
      ::::: ::::: ||| |||
39 LeuLeuLeuAlaPheValProPheArgLeuArgAspLysLeuThrG 55
      ::::: ::::: ||| |||
120 CCGCGTCGACATCTGCGCTTTTACCTTTTAAAGGAGACGCGCGCGCA 169
      ::::: ::::: ||| |||
55 yLysLeuGlyLleTrpLleGlyHisLysAlaLysLysGlnArgTrpArg 72
      ::::: ::::: ||| |||
170 TCGTCGCCATATGCGTCAAGCA.....GCGATGATCCCGAC 207
      ::::: ::::: ||| |||
72 LAGLThrLysLeuGlnTrpGlyPheProHisTrpThrGlnGlnArg 88
      ::::: ::::: ||| |||
208 CCGAAACGCTCAAGCGCTTTTTCGGAACGCGCAAGGCGGTTTGA 257
      ::::: ::::: ||| |||
89 GlnGlnValLleAspLysMetPheAlaValAlaGlnValMetPheG 105
      ::::: ::::: ||| |||
258 ACTTGGCCCCGCGTTTTCAGAAAACCGAGACATAGAACATGTCA 307
      ::::: ::::: ||| |||
105 yLleGlyGlnLleAlaLleArgSerLysLysHisLeuGlnLysArgSerG 122
      ::::: ::::: ||| |||
308 AAGCGTACAGCGCTGCGGAACATGTCACAGCGCTTTGGACACAGCA 357
      ::::: ::::: ||| |||
122 Lurhelle...GlyLeuGlnHisLleGlnAlaLysLleGlnLys 137
      ::::: ::::: ||| |||
358 GCGCTCATATTCATCAGCGGACATCGGACGCTGATTTGGCGGAG 407
      ::::: ::::: ||| |||
138 AsnLleLleLeuMetValProHisGlyTrpAlaLleAspLaserGly 154
      ::::: ::::: ||| |||
408 CTGATCAGCGAGCGCTTCGCTCCGCGTGAACCGGATGTCACAAACGC 457
      ::::: ::::: ||| |||
154 eLleLeuHisThrGln...GlyMetProMetThrSerMetLysAsnProH 170
      ::::: ::::: ||| |||
458 CGAAATTCAGAGCATAGACAAATCATGACAGGCGGAGGTTGCGGCG 507
      ::::: ::::: ||| |||
170 LsArgAsnProLeuValAspTrpLeuTrpThrLleThrArgGlnArgPhe 186
      ::::: ::::: ||| |||
508 AAGGAAAAACCGCGCTTACACATACAGAGGCGTCAACAAATCATCA 557
      ::::: ::::: ||| |||
187 GlyGlyLysMetHisAlaArgGln...AsnGlyLleLysProPheLeuSe 202
      ::::: ::::: ||| |||
558 AGCGCTGCTGCGGCGAAGCAACCAATCGCTGCGCGGACGACGCTCC 607
      ::::: ::::: ||| |||
202 HisValArgLysLysLysLysLysLysLysLysLysLysLysLysLys 215
      ::::: ::::: ||| |||
608 CCGCTCAGAGAGCGG.....GAGGCGTATGCGTGGATTTCTTCGCG 651
      ::::: ::::: ||| |||
216 .....GlnAspPheGlyAlaGlnGlnSerValPheValAspPhePheGly 230
      ::::: ::::: ||| |||
652 AAACCTGCGTATACCATAGCGCTGCGGCAAAATTCGACACGCTC...AA 698
      ::::: ::::: ||| |||
231 ThrTrpLysAlaThrLeuProGlyLysAlaHisLysMetAlaLysLeuSer 247
      ::::: ::::: ||| |||
699 AGCGGTGAAAAACCTGTTTCTGCTGCGAAGCGCTCCCTGCGGAGCAAG 748
      ::::: ::::: ||| |||
247 LsAlaValValLleProMetPheProArgTrpAsnAlaGlnLysGlyLys 263
      ::::: ::::: ||| |||
749 GTTTCGATTTGACATCGCGCGCTCCAGAGGAGATGAGAGCGGAGCAAA 798
      ::::: ::::: ||| |||
264 ...TyrgLysMetGlnLleHisProAlaMet...AsnLysSerAspAspPro 278
      ::::: ::::: ||| |||
799 GCCCATGATGCGCGCGTTCACACGCAATGCGCAATATTCGATTCGCGG 848
      ::::: ::::: ||| |||
279 GlnGlnSerAlaArgAlaMetAsnGlnGlnLleLysLeuThrPheValThr 295

```

849 TTTCCGACGACATCTGTTATG 873
 295 oalaprogluInTyrrValtriple 303
 seq_name: p1r2:E71569

seq_documentation_block:
 Probable acyltransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C:Species: Chlamydia trachomatis
 C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
 C:Accession: E71569
 R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A:Reference number: A71570; MUID:99000809
 A:Accession: E71569
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <ARN>
 A:Cross-references: GB:AE001275; GB:AE001273; NID:g3328388; PIDN:ACG67600.1; PID:g332839
 A:Experimental source: serotype D, strain UW-3/Cx
 A:Genetics:
 A:Gene: htrB

alignment_scores:
 Quality: 172.50 Length: 342
 Ratio: 1.033 Gaps: 12
 Percent Similarity: 48.830 Percent Identity: 23.977

alignment_block:

US-09-303-518d-569 x E71569 ..

Align seg 1/1 to: E71569 from: 1 to: 455

```

22 CGTTTCCCTTGGCAACGGCCATGCACATCCCTGTTGACCCCTG.. 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2  LeuphelsArgLeuArgThrGlyLeuValAspHisLeuVala 18
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
70 .....CTCAAAATGCCTCTCCCTGCTGCCGCTT 97
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 LTyrglyLeuGlyLeuGlyValLeuThrIleLeuArgLeuLeuProba 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
98 CCTGCTGCACACGCTGGAAACGGCTCGACATCTGGCTTTTACCTT 147
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 erSerLeuArgLeuPheSerIleGlyThrAlaLeuPheTyrphe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
148 TTAAGGAAGACCGCGCGCATGCTGCCCAATATG..... 183
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 IleSerAspValArgLysThrAlaLeuThrAsnLeuAlaLeuAlaPhe 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 .....CGTCAGGCA..... 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 oGluSerPheAlaGluArgTyrGlnIleAlaArgGlnSerValGln 85
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 .....GGCATGAATCCCGACCCCAAAACGGTCAAA 222
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
85 lmetIleIleThrPheValGluLeuAlaThrValAspLysPheAlaLys 101
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
223 GCCGTTTTCGGAACGGCAAAAGCGGTTTGGACTTGCCGCC.....GC 269
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
102 HisIleAspGluMetIleAlaIleAlaThrSerIleAspAlaProGlu 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
270 GTTTTTCGAACCGGAGACATAGAAACAATGTTCAACGGCTACAG 319
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 yPhePhe.....ProGluGluValSerGlnGlnGluLeu..... 130
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
320 GCTGGACATGTCAGAGCTTTCGACAAACGACGAAGGCTGCTATTC 369
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131 .....AspHisPhePheSerArgLeuAspArgGlnGluValAlaIle 145
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
370 ATCAGCGCGCACATCGCAGCTACGATTTGGCGGACGCTACATCAGCA 419
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

146 PheCysGlyHisGlnAlaAsnTrpGluLeuProPheLeuTyrIleThr 162
420 GCAGCTTCCTCCGTCGACGCCCATGTACAAACCGCGGAATCAAG 469
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
162 sArg.....TyrProGlyLeuAlaPheAlaIleProValLysAsnArg 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
470 CGATGACAAATATCATGACGGCGGAGGTTCCCGCAAGAAACACC 519
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
177 rGluAsnGlnLysIleIleSerLeuArgGluSerPheGlnGlyLysIle 193
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
520 GCGCTTACACATACAAAGGGTCAACAAATCATCAAGCCCTGCGCTC 569
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 ValProGln...AsnAlaIleAsnGlnAlaLeuArgAlaHisArg 209
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
570 GGGCGAAGCAACATCGTCTGCGCCGACACGTCCTCCCTCAAGAG 619
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
209 gGlyGluValValGlyIleValGlyAspGlnValLeuLeuSerSerLut 226
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
620 GCGGGGAAGGGGTATGGTGATTTCTTCGCAACCTGCTATACATG 669
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
226 ySer.....TyrProLeuPheGlySerGlnAlaPheThrThr 238
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
670 AGCTGGCGCAAAATTCGACACGTCMAAGCGTGAACCCGTGTTT 719
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 ThrSerProAlaLeuAlaIleTyrLysThrLysLysThrValIleAla 255
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
720 CTGCTGCAGACGCTGCTGCGGACAGGTTTCGATTTGCATCGCGC 769
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 lAlaIleTyrArgLysProAsnGlyAsnTyrLeuVal..... 268
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
770 CCGTCAAGGGGAATGACGGCGCAACCCCATGATGCCGCGCTTC 819
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
269 .....ProSerLysAlaPhe 273
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
820 AACCGCAATCCGAATATGATGATACG..... 846
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 HisAlaAsnThrGluLeuSerIleArgGluSerThrGluGlnLeuMet 290
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
847 .....CGTTT.....CGAGCGCAGT 862
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
290 pArgLeuMetArgPheLeuGluLysGlyIleThrCysLysProGluGln 307
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
863 ATCGTTTATGTACAAACCGCTACAA 888
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
307 rPheutPleuHisLysArgTyrLys 315
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq_name: p1r2:E71631

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase (htrB) RP718 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: E71631
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499
 A:Accession: E71631
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-290 <AND>
 A:Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15149.1; PID:e134
 A:Experimental source: strain Madrid E
 A:Genetics:
 A:Gene: htrB; RP718

alignment_scores:
 Quality: 169.50 Length: 206
 Ratio: 1.274 Gaps: 9
 Percent Similarity: 64.563 Percent Identity: 22.816

alignment_block:

US-09-303-518D-569 x E71631 ..

Align seg 1/1 to: E71631 from: 1 to: 290

```

289 GACATAGAACATGTTCAAGCGGTACAGCGGTGAGACATGTGACGA 338
   |||||
95 GluLeuGluSerArgIleGluIleIle...GlyIleGluSerIleValMet 110
   |||||
339 GCGTTTGACAAACAGCAAGGCGTGTATTCATCAGCCGACATCGCGCA 388
   |||||
110 sleuGluasp.....GlnProPheLeuPheSerGlyHisPheAla 125
   |||||
389 GCTAGCATTTGGGGGAGCGGTACATCAGCCGACGCTTCGCTCCCGCTG 438
   |||||
125 snTPASPILeserLeuValIleuValIleuValIleuValIleuVal 140
   |||||
439 ACCGCGATGATCAAAACCGCGCAAAATCAAGCATAGCAAAATCATGCA 488
   |||||
141 AlaValIleTyrArgIleValIleAsnAsnProTyrValAsnIleValAs 157
   |||||
489 GCGGCGAGCGGTGCGCGCAAGAAAGCGCGCTACACCATACAG 538
   |||||
157 nGluSerArgIleGluValIleuValIleuValIleuValIleuVal 174
   |||||
539 GCGTCAACAAATCATCAAGCGGTGCGCGCAAGCAACCATCGTC 588
   |||||
174 IlyIleArgSerLeuValIleuValIleuValIleuValIleuValMet 190
   |||||
589 CTGCGCGACACAGTCCTCCCTCAGAGAGCGGAGCGGTATGGGT 638
   |||||
191 LeuValAsp.....GlnIleMetAsnAspGlyIleGluVal 202
   |||||
639 GGATTTCTTCGCGCAACCTGCTATCATCATGACGTCGCGCAAAATGCG 688
   |||||
202 IProPheLeuGlyArgProSerMetThrAlaSerIleAlaIleValMet 219
   |||||
689 CACACGTCAAAGCGGTGAAACCGCTGTTTCTGCTGCGAAAGCGCTG... 735
   |||||
219 Ia.....LeuGlnTyrIleTyrProIleIleProCysGlnIleIleVal 233
   |||||
736 CCGTGGCGGACAAAGTTTGCATTTGCACATCGCGCCC...GTCCAAAGGGA 782
   |||||
234 ThrIleGlySerTyrPheIleValIleValIleuValIleuValIleuVal 250
   |||||
783 ATTGAACGCGCAACAAGCCCATGATGCC.....GCCGTGTTCACACCGCA 826
   |||||
250 uGlnThrGlyAspAsnIleValIleuValIleuValIleuValIleuVal 267
   |||||
827 AT.....GCCGAATATTTGATACCGCGTTTCCGACGCGATATGTTT 870
   |||||
267 snGlnIleLeuGlyIleuValIleuValIleuValIleuValIleuVal 283
   |||||
871 ATGTACAAACCGGTACAAA 888
   |||||
284 PheHisAsnArgTyrIle 289

```

seg_name: plir2:F81720

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase, probable TC0278 [Imported] - Chlamydia mu
 C:Species: Chlamydia muridarum, Chlamydia trachomatis Morn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C:Accession: F81720
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis Morn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150253
 A:Accession: F81720
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-453 <TE>
 A:Cross-references: GB:AE002295; GB:AE002160; NID:g7190314; PID:AAF39146.1; PID:g719031

A:Experimental source: strain N19g (Morn)
 C:Genetics:
 A:Gene: TC0278

alignment_scores:
 Quality: 164.50 Length: 336
 Ratio: 0.962 Gaps: 14
 Percent Similarity: 50.893 Percent Identity: 24.702

alignment_block:
 US-09-303-518D-569 x F81720 ..

Align seg 1/1 to: F81720 from: 1 to: 453

```

22 CTTGTTCCCGCTTGGAGACCGCATGACATCTGTTG..... 60
   |||||
2 LeuPheLysMetLeuArgSerGlyValIleuValIleuValAspHisLeuVal 18
   |||||
61 .....ACCGCTGCTCAATGCTTCCTCCCTGCGGCTT 97
   |||||
18 IlyGlyLeuGlyLeuGlyIleLeuThrIleLeuArgLeuLeuProArg 35
   |||||
98 CTTGTCGACACGCTGGGAAACCGGCTGCGACATCTGCGCTTTACCTT 147
   |||||
35 erSerLeuGlnLeuPheGlyLysGlyLeuGlyThrThrIlePheIleVal 51
   |||||
148 TTAAGAGAACCGCGCGCGCATCTGCGCAATATGCTGACGCAAGCAT 197
   |||||
52 IleSerAspPheArgIleThrAlaLeuThrAsnLeuAlaLeuAla.... 66
   |||||
198 GAATCCCGACCC.....AAAACGG 217
   |||||
67 .PheProGlyLysSerPheThrIleArgTyrGlnIleAlaLeuLysSerV 83
   |||||
218 TCAAGCGCTT.....TTGCGGAAACGCAAA..... 246
   |||||
83 alGlnGlnValIleIleThrPheIleGluLeuAlaThrValAspLysPhe 99
   |||||
247 .....GGCGTTTGGAACCTTCCCG 266
   |||||
100 AlalysHisIleAspGlnIleIleThrIleAlaSerSerGluAspAla 116
   |||||
267 C...GCGTTTTCAGAAACCGGACAGATAGAAACATGTTCAACGCG 313
   |||||
116 oGluGlyPhePhe.....ProGluGlnValSerSerGlnGlnLeu. 130
   |||||
314 TACACGCGCTGGAACATGTGCACAGCGCTTGGACAAACGAGGCGTG 363
   |||||
131 .....AsnAsnPhePheSerArgLeuAspGlnGlnGlnIleVal 143
   |||||
364 CTATTTCACAGCGCGCATCGGACGATGATTTGGCGGACGCTACAT 413
   |||||
144 IleLeuPheCysGlyHisGlnAlaAsnTyrGlnLeuProPheLeuVal 160
   |||||
414 CAGCGACGAGCTTCCGCTCCGCGACGCGCATGTCAAAACCGCGAAA 463
   |||||
160 eThrLysArg.....TyrProGlyLeuAlaPheAlaLysProValLys 175
   |||||
464 TCAAGCGATAGACAAATCATGACGCGGAGGCGGTGCGGCAAGCA 513
   |||||
175 snProArgLeuAsnArgIleIleSerLeuArgIleuValIleuValIleuVal 191
   |||||
514 AAAACGCGCTTACCATCAACAGGAGGTTCAACAAATCATCAAGCGCT 563
   |||||
192 LysIleValProGln.....AsnAlaIleAsnGlnAlaLeuArgAla 207
   |||||
564 GCGTTGCGGCGAAGCAACATCGCTGCGGACGACGCTCCCTCCCTG 613
   |||||
207 uHisLysGlyGlnValValGlyIleValIleValAspGlnValLeuLeu 224
   |||||
614 AAGAGCGGCGGAGCGGTATGGGTGATTTCTTGGCAAAACCTGCTAT 663
   |||||

```



```

224 erGlnTyrSer.....TyrProLeuPheGlySerGlnAlaPhe 236
664 ACCATGACGCTGGCGCAAAATGTCACACGATCAAGGCGTGAACCCCT 713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
237 ThrThrThrSerProAlaLeuLeuAlaIleTyrThrArgLysProValIle 253
714 GTTTTCTGCTGCGAAGCGCTGCTGGCGGACA..... 747
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
253 eAlaValAlaIleTyrArgGlnProAsnGlyAsnTyrLeuValAlaPro 270
748 .....GGTTGCAATTCACATCCGCCCTCCAAAGG 780
270 erLysAlaPheTyrAlaAsnThrGlnLeuSerIleArgLysSerThrGlu 286
781 GAATTGAACGGCGCAAGCCCATGATGCGCGCGTGTCAACCGCAATGC 830
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
287 GlnLeuMet...AspLys.....LeuMetArgPheLe 296
831 CGAATATTGGATACGCGCTTTTCCAGCGCATGCTTTATGTACAAAC 880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
296 uGlnLysGlyIleAlaCysLysProGlnGlnIlePheLeuHisLysA 313
881 GGTACAAA 888
313 rqrTyrLys 315

```

seq_name: p1r2:AG0251

```

seq_documentation_block:
  Lipid A biosynthesis acyltransferase (EC 2.3.1.-) [Imported] - Yersinia pestis (strain O
  C:Species: Yersinia pestis
  C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
  C:Accession: AG0251
  R:Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
  deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
  11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
  Nature 413, 523-527, 2001
  A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
  A:Reference number: AB0001; MID:21470413; PMID:11586360
  A:Accession: AG0251
  A>Status: preliminary
  A:Molecule type: DNA
  A:Residues: 1-320 <KUR>
  A:Cross-references: GB:AL590842; PIDN:CAC90875.1; PID:g15980074; GSPDB:GN00175
  C:Genetics:
  A:Gene: msbB
  C:Keywords: acyltransferase

```

```

alignment_scores:
  Quality: 158.50      Length: 288
  Ratio: 1.023         Gaps: 12
  Percent Similarity: 53.819      Percent Identity: 23.958

```

alignment_block:
US-09-303-518d-569 x AG0251 ..

Align seg 1/1 to: AG0251 from: 1 to: 320

```

70 CTCAAAATGCTCTCTGCTGCTGCTTCTGCTGCAACGCGTGGAAA 119
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 IleAlaIleAlaLeuAlaIleTyrIleProPheArgAspProLeuAla 50
120 CCGGCTCGACATGCTGGCGTTTACCTTTAAAGAAAGCCGCGCGCA 169
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
50 aglyIleIleArgLeuAlaGlyLysPheAlaIleTyrSerAlaArgLysArg 67.
170 TCGTCGCAAT.....ATGCGTCAGGACGACGATCCCGAC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 IaaArgIleAsnLeuLeuTyrCysMetProGluLeuProGluSerGluArg 83
208 CCCAAACGGTCAAAAGCGTTTTCGGAACGCAAAAGCGGTTTGA 257
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

84 GlnHisIleIleAspGlnMetPheAlaThrAlaIlePheLeuMet 100
258 ACTGCCCCCGCGTTTTCAGAAAAACCGAAGACATAGAAACAATTGCA 307
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100 tMetAlaIleLeuLysPheArgAspProLysLysValLeuThr..... 114
308 AAGCGTCAAGCGCTGGGAACATGTGCACAGCGCTTTGGAC..... 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 ..ArgValHis...Tyr...HisGlyGlnGluIleAspGluLeuGln 128
349 ..AAACAGAAAGGCTGTATTATCATCGCGCGACATCGGACGTACGA 395
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 GlnGlnGlnArgAsnValIleLeuLeuValProHisAlaTrpSerIleAs 145
396 TTTGGCGGAGCTTACATACACGACAGCTTCCGCTCCGCTGACCGCA 445
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145 rIleProAlaMetLeuLeuAlaGlnGln...GlyLysProValAlaGly 161
446 TGTACAAACCGCGCAAAATCATCAAGCGATAGCAAAATCATGACGGCGC 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
161 eTrpHisHisGlnArgAsnProLeuValAspTyrLeuTrpAsnSerAla 177
496 AGGCTTCGCGCAAGGAAAAACCGCGCTACGACGATACAGGCGTCA 545
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 ArgLeuHisPheGlyGlyArgIleHisAlaArgGln...SerGlyIle 193
546 ACAATCATCAAAAGCCCTGCTGGCGGCAAGCAACCATGCTGCGCCG 595
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 sProPheIleSerSerValArgGlnGlyPheTyrGlyTyrTyrLeuPro 210
596 ACCAGCTCCCGCTCCGCAAGGCGGGAAGCGGATGCGGCTTC 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
210 spGlnAspTyrGlyProGln.....GlnSerGluPheValAspPhe 223
646 TTGGCAAAACCTGCTATACCATGACGCTGGCGCAAAATTTGCACACGT 695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
224 PheAlaThrTyrLysAlaThrLeuProAlaIleGlyArgLeuMetLysA 240
696 C.....AAGCGCTGAACCCCTGTTT.....TTTGCTGCG 727
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 LysAlaGlnAlaIleValProMetPheProValTyrAsnTyrArgGln 257
728 AACGCTGCTGCGCGGACAGGTTTGCATTTGCATCGCGCGCGTCA 777
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
257 tsArgLeu.....AspIleTyrIleArgPropromet 267
778 GGGGAATTG...AACGGCGCAAAAGCCCATGATGCGCGCTGTCAACG 824
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
268 AspAspLeuAlaAspAlaAspAlaTyrIleAlaArgArgMetAsnG 284
825 CAATGCGCAATATTGATACCGCGCTTCCGACGCGATGCTTATGT 874
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
284 uGlnValGlnLeuLeuValLysProAsnProGlnTyrThrTrpIle 301
875 ACAACCGTACAAA 888
    : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 euLysLeuLeuLys 305

```

seq_name: p1r2:AE3391

```

seq_documentation_block:
  Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) [Imported] - Brucella melit
  C:Species: Brucella melitensis
  C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
  C:Accession: AE3391
  R:DeIvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
  .; Mazur, M.; Goldsman, E.; Selkova, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
  Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
  A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
  A:Reference number: AD3252; PMID:11756688
  A:Accession: AE3391
  A>Status: preliminary
  A:Molecule type: DNA

```

A;Residues: 1-307 <R>
 A;Cross-references: GB:AE008917; PIDN:AA152296.1; PID:g17983087; GSPDB:GN00190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME1115
 A;Map position: I
 C;Keywords: acyltransferase

alignment_scores:
 Quality: 152.50 Length: 330
 Ratio: 0.902 Gaps: 13
 Percent Similarity: 51.212 Percent Identity: 23.636

alignment_block:
 US-09-303-518D-569 x AE3391 ..

Align seg 1/1 to: AE3391 from: 1 to: 307

```

1 ATGTTGCTTACATTCAGGCTGTTCCCTTGGCAGCCGATGCA 50
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetPheLysLeuLysLeuLeuLeuPheArgTrpSerArgLysLeuLysG 17
51 CATC.....CTGTTGACGCGCTGCTCAAAATGCC 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 nPheasnTrpLeuTrpAlaGlnAlaValPheValLeuLeuGlyPheL 34
80 TCTCCCTGCTGCGCTTTCCTGCTGACAGCGTGGAAACCGCTCGGA 129
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 euArgLeuPheProAlaLysAlaAlaIleSerPheSerAlaArgValAla 50
130 CATCTGGCGTTTACCTTTTAAAGAGACGCGCGCGCATCGTGCACCA 179
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ArgLeuLleGlyProLeuThrProArgHisLysVal...AlaThrAspAs 66
180 TATGGCTGACGAGCATGATCCGACCCCAAAACGGTCAAAAGCGCTT 228
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 nLeuArgLysAla....TyrProGlnLysSerGlnAlaGlnLleValL 81
229 .....TTTGGCGGAACG 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 ysLleAlaArgGlnMetTrpAspSerMetAlaArgLeuPheAlaLutyr 97
241 GCAAAAGCGGTTTGGAACTTGCCTCCCGCTTTTCAGAAAAACCGAGA 290
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
98 .....IlePheLeuAspAlaValPheAspPheAspProTyrAl 110
291 CATAGAAACATGTTCAAGCGGTACACGCGTGGAAACATGTGCAGCAGG 340
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
110 aValLysProGlyLeuValGlnValGlnLysLleProLlePheGlnLysL 127
341 CTTTGGCAAAACAGCAAGCGGCTATTCATCAGCGCGTGCAGCAGCAGC 390
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 euArgLysPheLysLysProHisLlePhePheThrAlaHisThrLysL 143
391 TAGGATTTGGCGGAGCGTACATCAAGCAGCAGCTTCCG..... 429
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 PheGlnLeu.....LeuProLleCysAlaAl 152
430 .....TTCCCGCTGACCGCATGTACAAACCGCGGAAATCAAG 469
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
152 aThrPheGlyLysLeuAsnValThrAlaLeuPheArgProProAsnAsnProT 169
470 CGATA...GACAAATCATGACAGGCGGCGGCTTCGCGCAAGAGAA 516
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 yTrlLeuAsnLysValLeuLysAlaArgArgThr...AsnMetGlyHis 184
517 ACCGCGCTACAGCATACAGGGGTCAAAACATCATCAAAAGCCCTGCG 566
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 LeuValProSerLysAlaGlyAlaAlaTrpAlaLeuAlaGlyLleLeu 201
567 TTCGGCGAAGACCATGCTCTGCGCCACCAACGTCCTCCCTCCAG 616
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

201 yAspGlyGlyAsnValGlyMetLeuValAsp.....GlnL 213
617 AAGCGCGGAGAGCCGATATGGATTTCTTGGCAACCTGCTATAC 666
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 yspSerArgGlyValProSerThrPhePheAsnArgProValLysThr 229
667 ATGACGCTGCGCGCAAAATGGCACACGTCAAGCGGTGAAACCTGTT 716
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
230 AsnProLeuLeuAlaLysLeuAlaArgGlnTrpAspCysAspValLysPr 246
717 TTTCGCTGCGAAGCGCTGCTGCGGACAGTTTCCATTGCAATC 765
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
246 oAlaArgCysLleArgLeuProGlyGlyArg...TyrArgLeuGlnLeuT 262
766 .....CGCCCGCTCAAGAGGAGATTAACGCGCAGC 795
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
262 yGlnArgMetGlnLeuProArgAspGlnSerGlyGlnLle.....Asp 276
796 AAGCCCATGATGCGCGCTTTCAGCCGCAATGCCGATATTGATACG 845
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 IleAsnAlaThrThrGlnLeuLeuAsnAspThrValGlnGlnTrpValAr 293
846 CCGTTTCCGACGACATATCTGTTATGTACAAACGCTAC 885
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
293 gGlnTrpProGlyGlnTrpMetTrpPheHisLysArgTrp 306
seq_name: p1R2:T42129

```

seq_documentation_block:
 probable acyltransferase (EC 2.3.1.-) - Escherichia coli plasmid p0157
 C:Species: Escherichia coli
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000
 R:Accession: T42129; T00321
 R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
 Nucleic Acids Res. 26, 4196-4204, 1998
 A:Title: The complete DNA sequence and analysis of the large virulence plasmid of Esc
 A:Reference number: Z22068; MUID:96391744
 A:Accession: T42129
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-343 <BUT>
 A:Cross-references: EMBL:AF074613; PIDN:ANC70097.1
 A:Experimental source: Strain EDL933; serotype O157:H7
 R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubo
 S.; Shinagawa, H.
 DNA Res. 5, 1-9, 1998
 A:Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemor
 A:Reference number: Z14127; MUID:98290540
 A:Accession: T00321
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 12-343 <MAX>
 A:Cross-references: EMBL:AB011549; NID:94589740; PIDN:BA031840.1; PID:93337081
 A:Experimental source: strain EHEC O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Genome: plasmid p0157
 A:Note: L7029
 C:Keywords: acyltransferase

alignment_scores:
 Quality: 151.00 Length: 286
 Ratio: 0.993 Gaps: 9
 Percent Similarity: 53.147 Percent Identity: 22.028

alignment_block:
 US-09-303-518D-569 x T42129 ..

Align seg 1/1 to: T42129 from: 1 to: 343

```

82 TCCCTGCTGCGCTTTCCTGCTGACAGCGTGGAAACCGCTCGGACA 131
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 AlaMetValProProAlaLeuArgAspProLeuLeuLysLysLeuGlyMe 83

```

```

132 TCTGGCGTTTACCTTTAAAGAGACCGCGCGCATGTCGCCAAT 181
133 ||||| ||||| ||||| ||||| ||||| |||||
83 tleuValIglYargLeuIglYysSerAlaArgIglAlaLeuIleIle 100
182 TGGCT.....CAGCAGCATGATCCGACCCCAAAAGCGTC 219
100 euseLeuCySPheProGluTyrSerAspIysGluSgluAsnIleVal 116
220 AAGCGCTTTTTCGGAAACGGCAAAAGCGTTTGAACTTGCCCGCC 269
117 AspAlaMetPheAlaThrAlaSerMetAlaValLeuMetAlaGlu 133
270 GTTTTTCAGAAAACCGAAGACATAGAAACATGTTCAAGCGGTACAG 319
133 uAlaLeuSerGlyProAspIysIleSerHisArgIleArg...TyrAsnG 149
320 GCTGGAGACATGTCGACGAGCGTTTGACAAACAGCAGCGCTATTTC 369
149 IyLeuGluIleValIglYsMetAlaGlnAsnAsnGluIyValIlePhe 165
370 ATCAGCGCGCACATCGCAGCTACGATTG..... 399
166 leuValIProHisAlaIleTrrpIyAlaSPleProAlaMetLeuMetAla 182
400 .GGCGGACGCTACATCAGCCAGCAGCTTCCTCCGCGTACCGCATGT 448
182 aserGlyArg.....LysMetAlaIleMetP 191
449 ACAAAACCGCGCAAAATCAAGCATAGCAAAATCATGCGAGCGCGGAG 498
191 heHisAsnGlnArgAsnProValIleAspTyrValITrrpSerValArg 207
499 GTTCCGCGCAAGAAACCGCGCTACCGACATACAAAGGGGTCAACA 548
208 ArgGlyPheGlyIyLysLeuHisAlaArgAsn...AspGlyIleAlaSer 223
549 AATCATCAAGCGCTGCGTGGGGAAGCAACCATGCTGCTGCC.... 594
223 rPheValArgSerValArgGlnGlyTyrTrrpIyTyrTrrpLeuProAspG 240
595 ..GACCCAGTCCCTCCCTCAAGAGCGGGAAGCGGTATGGGTGAT 642
240 IAspHisGlyProGluPheSerGlu.....PheAlaAsp 251
643 TCTTCGCGCAACCTGCTATACATGACGCTGGCGCAAAATTTGGCACA 692
252 PhePheAlaThrTyrLysAlaIleThrLeuProValIleGlyArgLeuSerAr 268
693 CGTCAAGCGGTGAAGACCTGTGTTTCTGCTGGCAAGCGCTGCTGGCG 742
268 gIleSerGlyAlaArgIleIle.....ProLeuPheProValT 281
743 GACAAGGT.....TTCGATTTCACATCCGCGCGTCCCAAGG 780
281 yAspGlyLysThrHisIleThrIleHisValSerProProLeuAla 297
781 GAATGACGCGGACAAAGCCCATGATGCCCGCTGTCAACCCGCAATGC 830
298 ILeuArgIlyLysSerAspAlaHisIleAlaArgClnIleAsnGluVala 314
831 CGAATATGATACGCGCTTTTCGACGACAGTATCTGTATTATGACAAAC 880
314 IGlAsnPheValArgProHisProGluGlnTyrThrTrrpLeuLysL 331
881 GCTACAA 888
331 euleLys 333
seq_name: p1r2:C97836
seq documentation block:
hypothetical protein htrb [imported] - Rickettsia conorii (strain Malish 7)

```

```

C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97836
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: C97836
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL03629.1; PID:g15620214; GSPDB:GN00173
A:Gene: htrb

alignment_scores:
Quality: 149.00 Length: 201
Ratio: 1.221 Gaps: 8
Percent Similarity: 60.697 Percent Identity: 23.383

alignment_block:
US-09-303-518D-569 x C97836 ..

Align seg 1/1 to: C97836 from: 1 to: 290

310 GCGGTACACGCGCTGGAAACATGTGACAGAGGCTTTGGACAAACAGAG 359
101 ||||| ||||| ||||| ||||| ||||| |||||
101 AlalleIleGlyIleGluAsnIleLys.....LysLeuGluIgl 113
360 G.....CTGCTATTTCATCAGCGCGCACATGCGAGCTAGAGTATTTGGCG 403
113 yGlnProPheLeuLeuPheGlyIyGlnHisPheAlaAsnITrrpSPleSerI 130
404 GACCTACATCAGCCAGCAGCTCCGTTCCCGCTGACCGCATGTACAA 453
130 IeLysIleLeuHisLysPheTyrPro...LysValAlaValIleTyrArg 145
454 CCGCGCAAAATCAAGGATAGCAAAATCATGCAAGCGCGGAGGTTGC 503
146 LysAlaAsnAsnProTyrValAsnLysLeuValAsnGluSerArgAlaG 162
504 CGGCAAGAAACCGCGCTACACATACAAAGGGGTCAACAATCA 553
162 yAspLysLeuArgLeuIleProLysGlyProGluGlySerArgAlaLeuY 179
554 TCAAGCGCTGCGTGGGGAAGCAACATGCTGCTGCCGCAACGCTC 603
179 AlrPheAlaIleLysGluSerGluSerIleValIleMetLeuValAsp..... 193
604 CCTCCCTCAAGAGCGGGAAGCGGTATGGGTGATTCTTGGCAA 653
194 .....GlnLysMetAsnAspGlyIleGluValIleProPheLeuGlyH 207
654 ACCTGCTTATACATGACGCTGGCGCAAAATTTGGCACAAGTCAAGGCG 703
207 sProAlaMetThrAlaSerAlaIleAlaLysIleAla.....LeuGlnT 222
704 TGAAAACCTGTGTTTCTGCTGCAAGCGCTG...CCTGGCGACAAGT 750
222 yTrpLysTyrProIleIleIleProCysGlnIleIleArgThrLysLysTyr 238
751 TTGCAATTCGACATCCGCGCC...GTCAAGGGGAATTAGAGGCGACAA 797
239 PheLysValIleValHisProGlnLeuLysPheGluGlnIThrGlyAspAs 255
798 AGCCCATGATGCC.....GCCGTTCACACCGCAATGCCGAAT 835
255 nLysAlaAspCysTyrAsnIleMetLeuAsnIleAsnGlnMetLeuGlyG 272
836 ATTGATACGCGCTTTTCGACGACAGTATCTGTATTATGACAAACGCTAC 885
272 IuTrpValLysGlnAsnProAlaGlnITrrpPheThrPheHisAsnArgITrp 288

```


299 aSerGlnProGlnGlnTrpMetTrpIleHisLysArgTrpLys 313

seq_name: p1r2:D97552

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase (hrb) rp718 [Imported] - Agrobacterium tum
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: D97552
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: AF7359; PMID:11743194
A:Accession: D97552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <KUR>
A:Cross-references: GB:AB007869; PIDN:AAK87373.1; PID:915156679; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_2930
A:Map position: circular chromosome

alignment_scores: Quality: 141.00 Length: 289
 Ratio: 1.007 Gaps: 14
 Percent Similarity: 48.443 Percent Identity: 23.183

alignment_block:

US-09-303-518D-569 x D97552 ..

Align seg 1/1 to: D97552 from: 1 to: 312

```

190 GCAGCGCATGATCCGACCCCAAAAGCGTCAAGCGTTTTCGCGAAGC 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
41 AlaglyIleArgAlaThrAspArgLeuAlaArgLeuIleGlyProLysTh 57
240 GCGCAAAAGCGCGTTTG.....GAACCTGCCCCCGCGTTTTCAGAA 280
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
57 rGlyArgHisLysLeuMetLeuTyrAsnLeuAlaArgAlaPheProGlu 74
281 AACCGGACATAGAACAAATGTTCAAGCGGTACAGCGCTGG..... 324
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
74 ysthGlnGlu...GluArgLeuAlaIleAlaMetAspSerTrpAlaasn 89
325 .....GAACATGTC..... 333
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 MetGlyArgLeuAlaIleGluTyrValPheLeuAspArgLeuPheAspPh 106
333 ..... 333
106 eAspProGluLysAsnGluProGlyArgIleGluValGlnGlyThrSerT 123
334 .....CAGCAGCGTTTGGCAAAACAGCAAGCGGTCTTTCATCAGCGCG 378
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
123 hrPheLeuGlnLeuAlaArgAspAsnProArgProPheIleValPheThrAla 139
379 CACATCGGCACCTAGATTGGCGGACGCTACATCAGCCAGCAGCTTCC 428
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140 HisSerGlyAsnPheGlnLeu.....LeuPr 148
429 G.....TTCGGCTGACCGCCCATCATGACAAACCGC 457
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
148 oValAlaGlySerAlaPheGlyLeuAspValThrValLeuPheArgProP 165
458 CGAAATTCAAAGCGATA...GACAAATCATCGAGCGGCGAGGCTTCGC 504
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
165 roAsnAspProTyrValAlaAspLysValPheAsnPheArgLysGluArg 181
505 GCGAAAGGAAACCGCGCTACACGATACAGGGGTCAACAAATCAT 554
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
182 ...MetLysAsnLeuValProSerHisAlaGlySerSerPheAlaLeuAl 197

```

```

555 CAAGCCCTGCGTTGGCGGAAGACACCATGCTCTGCCGACGACGCTCC 604
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
197 aArgGlnLeuGlnLysGlyGlyValGlyValGlnLeuValasp..... 211
605 CCTCCCTCAAGAGCGGGGAGCGGATGCGATGCGATTTCTTGGCAAA 654
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
212 .....GlnLysPheGlyLysGlyLeuThrThrLysPhePheGlyLeu 225
655 CTGCGCTATACCATGACGCTGGCGGCAAAATTTGGCACACGTCAAGGCGT 704
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
226 GluValArgThrAsnProLeuAlaLysLeuValArg..... 238
705 GAAACCCCTGTTTCTGC.....TGCAGACGCTGC 736
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
239 .....GlnPheAsnLysAspValTyrProAlaArgCysIleArgLeuP 253
737 CTGGCGCAAGGTTTGCATTGTCATCCGCGCCCGTCGCAAGGGAATTG 786
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
253 roAspAsnArg...TyrArgLeuGlnIleGluPro...LysValGlnIle 267
787 .....AACGCGACAAAGCCCATGATGCCGCGCTGT 818
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
268 ProArgAspGlnLysGlyAsnValAspIleGlnAlaThrAlaGlnLeu 284
819 CAACCGCAATGCGGATATTTGATACGCCGTTTCCGACGACGATGTGT 868
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
284 uAsnAspLysValGlnSerTrpValArgGlnTyrProGlyGlnTrpLeu 301
869 TTATGTACMACCGCTAC 885
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 rPtyrHisAspArgTrp 306

```

seq_name: p1r2:AF2772

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase [Imported] - Agrobacterium tumefaciens (
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AF2772
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCl
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AF2772
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <KUR>
A:Cross-references: GB:AB006886; PIDN:AA142596.1; PID:917740022; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: msbB
A:Map position: circular chromosome

alignment_scores: Quality: 141.00 Length: 289
 Ratio: 1.007 Gaps: 14
 Percent Similarity: 48.443 Percent Identity: 23.183

alignment_block:

US-09-303-518D-569 x AF2772 ..

Align seg 1/1 to: AF2772 from: 1 to: 312

```

190 GCAGCGCATGATCCGACCCCAAAAGCGTCAAGCGTTTTCGCGAAGC 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
41 AlaglyIleArgAlaThrAspArgLeuAlaArgLeuIleGlyProLysTh 57

```

seq_documentation_block:
lipid A biosynthesis (kco)2-(lauroyl)-lipid IVA acyltransferase VC0212 [imported] - Vibrio
Species: Vibrio cholerae

[illegible]

863 ATCTGTTT 870
 |||
 299 yrmctrr 301
 seq_name: plr2:c82350

seq_documentation_block:

lipid A biosynthesis lauroyl acyltransferase VC0213 [Imported] - Vibrio cholerae (strain C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: G82350
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardon, D.; Esmailova, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: AB2035; MUID:20406833
 A:Accession: G82350
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-318 <HER>
 A:Cross-references: GB:AE004111; GB:AE003852; NID:99654614; PIDN:AAF93389.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 A:Gene: VC0213
 A:Map position: 1

alignment_scores:

Quality:	136.50	Length:	317
Ratio:	0.858	Gaps:	15
Percent Similarity:	50.158	Percent Identity:	24.921

alignment_block:

US-09-303-518D-569 x G82350 ..

Align seg 1/1 to: G82350 from: 1 to: 318

```

58 TTGACGGCCCTCTCAATGCTCCTCCTGCGCTTCTGTCGCA 107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
32 LeuLeuAlaLeuLeu.....ValasnLeuProTyrProValLeuLe 46
108 CACGCTGGGAAACCGCTCGA..... 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
46 uUyrlleGlyArGlyLeuGlyGlnPheSerMetArGheGlyLysTys 63
130 .....CATCTGGCGTTTACCTTTTAAAG 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
63 rGValHisIleAlaArGArGAsnLeuGluLeuAlaPheProThrMetSer 79
154 GAAGACCC.....GGCGGATGTCGCCCAATATGCGTCAGGACGCAT 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 GlnSerGluIleAspAlaPheValLeuGlnAsnPhelysAsnThrGly.. 95
198 GAATCCGACCCCAAAACGCTCAAGCCGTTTTCGGAAGGCAAAAG 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
96 .....AlaAlaLeuIleGluThrGlyIleT 104
248 GCGGTTTGAACTGCCCCCGCTTTTTCAGAAAACCGGAACATAGAA 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
104 hTTPPrPheTPrProThrTPrArGheLysArGlyLeuIleAspLysasp 120
298 ACAATGTTCAAGCGGTACACGCTGGGAACATGTGACAGAGGCTTGA 347
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 Thr.....GlnAlaIleAr 125
348 CAATCAC.....GAGGCGCTATTCATCAGCCGACATCG 385
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
125 gGlnHisAlaLysThrGlyGlnGlyValLeuLysCysValHisAlaL 142
386 GCAGCTACGATTGGCGGACGCTACATCAGCCAGCTCCGTCGCCG 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 euAsnLeuGluIleThrAlaArGAlaPheAla...ValLeuGlyIleGly 157

```

seq_name: plr2:T43023

seq_documentation_block:

ceoa protein - Burkholderia cepacia
 C:Species: Burkholderia cepacia
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 R:Charon, R.L.; Barry, J.J.; Burns, J.L.
 submitted to the EMBL Data Library, April 1997
 A:Reference number: Z22290
 A:Accession: T43023
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-405 <CH>
 A:Cross-references: EMBL:U97042; NID:92109269; PID:92109270; PIDN:AAB58160.1
 A:Experimental source: strain K61-3
 A:Gene: ceoa

alignment_scores:

Quality:	133.50	Length:	212
Ratio:	1.362	Gaps:	10
Percent Similarity:	46.226	Percent Identity:	28.774

alignment_block:

US-09-303-518D-569 x T43023 ..

```

436 CTGACCGCATGTACAAACCGCCGAAATCAAGCATAGCAAAATCAT 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
158 GlyTyrGlyValTyrArGProHisSerAsnProAlaTyrGluPheIleG 174
486 GCAGCGGCGGAGGTTCCGCGCAAGAAAACCGGCTTACCAACATAC 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 nTyrArGlyArGThrArGAsnGlyAsnGlnLeuIleAsnArGThr... 189
536 AAGGCTCAACAAATCATCAAGCCGCTGTGGGCGGCAACCATC 585
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 ..AspIleLysIleMetIleArGValLeuArGlnGlyValArGLeuPhe 205
586 GTCTGCCCCGACACCATGCTCCCTCCCTCAGAAAGGCGGG.....GAAG 629
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
206 TyrLeuProAsp.....GlnAspTyrGlyHisAsnLysSe 217
630 GGTATGGGTGATTTCTTCGGC...AAACTGCTTATACATGACGCTGG 676
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 rValPheValIProPhePheAlaValGluGluAlaCysThrThrThrGlyT 234
677 CGGCAAAATTTGCAACACGTCAAGCGCTGAAACCCGTGTTTCTGCTGC 726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
234 hrSerIleLeuAlaTyrThrSerHisCysAlaIleValIle..... 247
727 GAAGCCCTGCTGGCGCAAGATTTCGATTTGCATCCGCCCTGCA 776
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 .....GlySerGlyPhe.....ArgAsnAlaG 255
777 AGGG.....GAATTGAACGGCGCAAGGCCATGAT..... 807
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
255 nGlyArGtyrGluIleMetAlaAspLysSerIleGluAlaAspTyrProG 272
808 .....GCCGCGTGTCAACCGCAATGCCGATAT 837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
272 InLysAspGluThrAlaAlaAlaAlaTyrMetAsnLysPheValGluGlu 288
838 TGGATACGCGGTTTTCGAGCGAGTATCTGTTATGACAAACCGCTACAA 867
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
289 IleIleLeuArGAlaPheProGluGlnTTPMetLysThrLysArGhe 305
888 A 888
305 s 305

```



```

221 rghisArgGlyProGlyArgLeuLeuArgValProGluProValArgHis 237
609 ..... CCTCAAGAGCGGGGAG 628
238 HisArgGlyArgLeuLeuHisGlyHisGlyGlnAlaArgArgLeuGlnArg 254
629 GCGTATGGGTGATTTCTTCCGCAACCTGCGTATACCATGACGCTGGGG 678
254 gGlnAlaGlyGlyValArgGlnArgValAlaValSerArgArgHisGlyG 271
679 GCAAAATTGGCACACGTCAA..... 698
271 LysArgProGlnArgGlnAspLeuGlnProValProHisGlnProArg 287
699 AGCGGTGAAACCCCTGTTTTCGTGCGACAGCGCTGCGCGGACAG 748
288 ArgAlaArgHisPro.....Pro.ProProGlyArgH 298
749 GTTTCGATTTGACATCCGCCGTCGCAAGGGAAATTGAACGCGACAA 798
298 IsArgAspLeuArgLeuLeuHisValGlnArgGlnProGlnGlyGlnArg 314
799 ..... GCGCATGATGCCCGCTGTTCAACCCCATGCCGAATTATTCAT 842
315 ArgGlyAlaGlnLeuGlyAlaLeuLeuProGlnHisAla..... 327
843 ACGCGCTTTCCGACGACGATATCTG 867
328 AlaArgLeuProHisGlnLeuLeu 335

```

seq_name: p1r2:E90949

```

seq_documentation_block:
  heat shock protein Mabb [imported] - Escherichia coli (strain O157:H7, substrain R1MD 05
  C/Species: Escherichia coli
  C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
  C/Accession: E90949
  R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
  gaswara, N.; Yasunaga, T.; Kunara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
  DNA Res. 8, 11-22, 2001
  A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
  A:Reference number: A96629; MUID:21156231; PMID:11258796
  A:Accession: E90949
  A>Status: preliminary
  A:Molecule type: DNA
  A:Residues: 1-323 <NAV>
  A:Cross-references: GB:BA000007; PIDN:BA835988.1; PID:q13362033; GSPDB:GN00154
  A:Experimental source: strain O157:H7, substrain R1MD 0509952
  C/Genetics:
  A:Gene: ECs2565

```

```

alignment_scores:
  Quality: 129.50      Length: 297
  Ratio: 0.881        Gaps: 11
  Percent Similarity: 49.495  Percent Identity: 23.232

```

alignment_block:

US-09-303-518d-569 x E90949 ..

Align seg 1/1 to: E90949 from: 1 to: 323

```

64 GCGCGTCGAATGCTCTCCCTGCGCGCTTCTGTCGACAGCT 113
   |||.....|.....|.....|.....|.....|.....|
31 AlaAlaMetAlaGlyIleAlaLeuThrProProLysPheArgAspProI 47
114 GGAAGAACGCGCTCGACATCTGGCGTTTACCTTTTAAAGGAAGACGGC 163
   :|||.....|.....|.....|.....|.....|.....|
47 eleuAlaArgLeuGlnArgIleAlaGlyArgLeuGlyLysSerSerArg 64
164 GCGCGATGTCGCCAATATG..... 183
64 rGAlaGlnAlaLeuIleAsnLeuSerLeuGlyPheProGlnArgSerGlnAla 80

```

```

184 ...CGTCAGGCGAGCATGATCCGACCCCAAAAGCGTCAAGCGCTTT 230
   |||.....|.....|.....|.....|.....|.....|
81 GlnArgGlnAla.....IleValAspGlnMetPhe 90
231 TGGCGAAACGCGCAAAAGCGGTTTGGAACTTGCCCGCGCTTTTTCAGAA 280
   |||.....|.....|.....|.....|.....|.....|
90 eAlaThrAlaProGlnAlaMetAlaMetMetAlaGlnLeuAlaIleArg 107
281 AACCGAAGACATAGAACAAATGTTCAAAAGGCGTACACCGCTGGACAT 330
   |||.....|.....|.....|.....|.....|.....|
107 LyrProGlnLysIleGlnProArgValAsp...TrpGlnGlyLeuGlnIle 122
331 GTGACGAGCGCTTTGACAAACAGCAAGGCGCTGATTCATACAGCGCGCA 380
   |||.....|.....|.....|.....|.....|.....|
123 IleGlnGlnMetArgArgAsnAsnGlnLysValIlePheLeuValProH 139
381 CATGCGCAGCTACGATTTGGCGGACGCTACATACGACGACGCTTCCT 430
   |||.....|.....|.....|.....|.....|.....|
139 SGlyTrpAlaValAspIleProAlaMetLeuMetAlaSerGln...Gly 155
431 TCCGCTGACCCCATGTACAAACCGCGAAATCAAGCGATGACAA 480
   |||.....|.....|.....|.....|.....|.....|
155 LInLysMetAlaAlaMetPheHisAsnGlnGlnAsnProValPheAspTyr 171
481 ATCATGACAGCGCGGCGAGGTTCCGCGCAAAAGAAACCGCGCTACAG 530
   |||.....|.....|.....|.....|.....|.....|
172 ValTrpAsnThrValArgArgArgPheGlyGlyArgLeuHisAlaArg 188
531 CATCAAGGGGTCAACAAATCATCAAGCGCTGCGTTCGGCGCAAGCA 580
   :|||.....|.....|.....|.....|.....|.....|
188 n...AspGlyIleLysProPheIleGlnSerValArgGlnGlyTyrTrp 204
581 CCATGCTCTGCTCC.....GACCACTGCCCTCCCTCAAGAGCGGG 624
   |||.....|.....|.....|.....|.....|.....|
204 LyrTyrTyrLeuProAspGlnAspHisGlyProGlnHisSerGln..... 218
625 GAAAGCGTATGGGTGATTTCTTCCGCAACCGTCCATACATGACGCT 674
219 .....PheValAspPhePheAlaThrTyrLysAlaThrProAl 232
675 GCGCGCAAAATTGGCACACGTCGCAAGGCGTGAACCGCTGTTTCTGCT 724
   :|||.....|.....|.....|.....|.....|.....|
232 AlIleGlyArgLeuMetLysVal.....Cys 241
725 GCGAAGCCCTG.....CTGGCGGACAGCT..... 750
   |||.....|.....|.....|.....|.....|.....|
241 rGlnAlaArgValAlaProLeuPheProIleTyrAspGlyLysThrHisArg 257
751 TTCGATTTGCACATCCGCGCGCTCAAGGGAA...TTGACGCGGACAA 797
   :|||.....|.....|.....|.....|.....|.....|
258 LeuThrIleGlnValArgProPheMetAspAspLeuGlnAlaAsp 274
798 AGCCCATGATCCGCGCTGTTCACACGCAATGCGCAATTTGATGACGCG 847
   |||.....|.....|.....|.....|.....|.....|
274 PHisThrIleAlaArgArgMetAsnGlnGlnValGlnIlePheValGly 291
848 GTTTCCGAGCGCAGTATCTGTTATGTACACCGCTACAA 888
   |||.....|.....|.....|.....|.....|.....|
291 rGArgProGlnGlnTyrThrThrIleLeuLysLeuLeuLys 304

```

seq_name: p1r2:A85798

seq_documentation_block:

```

  suppressor of htrb, heat shock protein [imported] - Escherichia coli (strain O157:H7,
  C/Species: Escherichia coli
  C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
  C/Accession: A85798
  R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
  Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanite, E.; Potamousis, K.; Apoda
  Nature 409, 529-533, 2001
  A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
  A:Reference number: A85480; MUID:21074935; PMID:11206551

```



```

N:Alternate names: membrane-bound lytic transglycosylase
C:Species: Escherichia coli
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A42608; IS4979; G64947
R:Karow, M.; Georgopoulos, C.
J. Bacteriol. 174, 702-710, 1992
A:Title: Isolation and characterization of the Escherichia coli msbB gene, a multico
A:Reference number: A42608; MUID:92121107
A:Accession: A42608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <KAR>
A:Cross-references: GB:M87660; NID:g146876; PIDN:AAA96706.1; PID:g146877
A:Experimental source: strain K-12, substrain W3110
A:Note: sequence extracted from NCBI backbone (NCBI:77416, NCBI:77418)
J:Engel, H.; Shink, A.J.; van Wijngaarden, L.; Keck, W.
J. Bacteriol. 174, 6394-6403, 1992
A:Title: Murein-metabolizing enzymes from Escherichia coli: existence of a second lyt
A:Reference number: IS4979; MUID:93015688
A:Accession: IS4979
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <RES>
A:Cross-references: GB:M87660; NID:g146876; PIDN:AAA96706.1; PID:g146877
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.D.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64947
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-323 <BAT>
A:Cross-references: GB:AE000279; GB:U00096; NID:g1788154; PIDN:MAC74925.1; PID:g17881
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: msbB; mlt
C:Function:
A:Description: transfers myristate or laurate, activated on ACP, to (Rdo)2-(lauroyl)-
A:Pathway: lipopolysaccharide core biosynthesis
A:Note: decanoyl, palmitoyl, palmitoleyl and (R)-3-hydroxymyristoyl-ACP are poor acy
C:Keywords: acyltransferase; lipopolysaccharide core biosynthesis; transmembrane prot
F:23-43/Domain: transmembrane #status predicted <TM1>
F:85-105/Domain: transmembrane #status predicted <TM2>
F:133-153/Domain: transmembrane #status predicted <TM3>

alignment_scores:
      Quality: 127.50      Length: 297
      Ratio: 0.867      Gaps: 11
      Percent Similarity: 49.495      Percent Identity: 23.232

alignment_block:
US-09-303-518D-569 x A42608 ..

Align seg 1/1 to: A42608 from: 1 to: 323

64 GCCCTGCTCAATGCTCTCCCTGCGCGCTTCTGCTGTGCACAGCT 113
||| :::: :::::|||| ||| ::::
31 AlAlaMetAlaGlyIleAlaLeuThrProProLysPheArgAspProI 47
114 GGGAAACGCGTCCGACATCTGGCGTTTACCTTTTAAAGAGACGGC 163
: ||||| ||||| ::::: ||| ||| ||| ::::: |||
47 eLeuAlaArgLeuGlyArgPheAlaGlyArgLeuGlyLysSerSerArg 64
164 CGCGCATGTCGCCAATATG..... 183
||| :::: ||| ::::
64 rGArGAlaLeuIleAsnLeuSerLeuGlySphProGluArgSerGluAla 80
184 ...CGTAGAGCAGGCAATGCCGACCCCAAAAGCGTCAAGCCGTTT 230
||| ::::: |||
81 GluArgGluAla.....IleValAspGluMetPh 90

```

```

231 TCGGAAAGCGCAAAAGCGGTTTGAACCTGCCCGCGCTTTTTCAGAA 280
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
90 eAlaThrAlaProAlaIleAlaMetAlaIleAlaIleArg 107
281 AACCGGAAGACATGTAACAATGTTCAACGGGTACACGGCTGGGAACAT 330
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 LyrProGluLysIleGlnProArgValAsp...TrrGlnGlyLeuGluIle 122
331 GTGCGACGAGGCTTTGACAAACAGAGGCGTGTATTCATCAGCGCGCA 380
: : : : : : : : : : : : : : : : : : : : : : : : : : :
123 IleGluIleMetArgAsnAsnGluLysValIlePheLeuValProH 139
381 CATCGGACGCTACGATTTGGCGGAGCGCTACATCAGCGCAGCTTCCGT 430
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
139 SGIYTRPAlaValAspIleProAlaMetLeuMetAlaSerGln...GlyG 155
431 TCCGCTGACCGCCATGTCACAAACCGCGCAAAATCAAGCGATAGACAA 480
: : : : : : : : : : : : : : : : : : : : : : : : : : :
155 LInysMetAlaIleAlaMetPheHisAsnGlnGlyAsnProValPheAsp 171
481 ATCATGCAAGCGGCGAGGCTTCGCGCAAAAGAAACCGCGCTACCGAG 530
: : : : : : : : : : : : : : : : : : : : : : : : : : :
172 ValTrpAsnThrValArgArgArgPheGlyGlyArgLeuHisAlaArgAs 188
531 CATCAAGGCGGTCAACAAATCATCAAAAGCGCGCTGTCGGCGAGCAAA 580
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
188 n...AspGlyIleLysProPheIleGlnSerValArgGlnGlyTrpG 204
581 CCATGCTGCTGCTGCC...GACCAAGTCCCTCCCTCAGAAAGCGGCG 624
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
204 LYTYRTrpLeuProAspGlnAspHisGlyProGlnHisSerGlu... 218
625 GAAAGCGATGCGGTGATTTCTGCGCAAAACCTGCTACCATGACGCT 674
: : : : : : : : : : : : : : : : : : : : : : : : : : :
219 .....PheValAspPheThrValThrTrpLysAlaThrLeuProAl 232
675 GCGCGCAAAATGTCGACAGCTCAAAAGCGGTGAAACCTGTTTCTGCT 724
: : : : : : : : : : : : : : : : : : : : : : : : : : :
232 AlIleGlyArgLeuMetLysVal.....CysA 241
725 GCGAAGCGCTG.....CCTGCGGACGAAAGT..... 750
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 rGAlaArgValValProLeuPheProIleTrpAspGlyLysThrHisArg 257
751 TTCGATTTGCACATCCGCCCGCTCCAGAGGAA...TTGAAGCGGACAA 797
: : : : : : : : : : : : : : : : : : : : : : : : : : :
258 LeuThrIleGlnValArgProPheMetAspLeuLeuGluAlaAspAs 274
798 AGCCCATGATGCGCGCGTGTTCACCGCAATGCCAATATTGATACGCC 847
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
274 PHisThrIleAlaArgArgMetAsnGluValGluIlePheValGlyP 291
848 GTTTTCGCGGAGCATGTATGTTATGATCAACCGCTACAAA 888
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
291 rArgProGluIleTrpThrTrpIleLeuLysLeuLeuLys 304

```

seq_name: plir2:AE0742

seq_documentation_block:

lipid A acyltransferase (EC 2.3.1.-) [imported] - *Salmonella enterica* subsp. *enterica* serovar typhi
 C:Species: *Salmonella enterica* subsp. *enterica* serovar typhi
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AE0742
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Koul, S.; O'Garra, P.
 Nature 413, 848-852, 2001.
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AE0742
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-323 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05640.1; PID:g1650136; GSPDB:GN00176
 C:Genetics:
 A:Gene: SRY2097
 C:Keywords: acyltransferase

alignment_scores:
 Quality: 127.50 Length: 290
 Ratio: 0.885 Gaps: 10
 Percent Similarity: 49.655 Percent Identity: 24.138

alignment_block:
 US-09-303-518D-569 x AE0742 ..

Align seg 1/1 to: AE0742 from: 1 to: 323

```

64 GCCCTGCTCAAAATGCTCTCTCTGCGCGCTTCTGTCACACGCT 113
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 AlaAlaMetAlaGlyIleAlaLeuThrProAlaSerPheArgAspProLe 47
114 GGGAAACCGGCTCGGACATCTGGCGTTTACCTTTTAAAGAAAGCGCG 163
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
47 uLeuAlaThrLeuGlyArgPheAlaGlyArgLeuGlyLysSerSerAla 64
164 CGCGCATGCTCGCAATATGCT.....CAGCGACGATGAAT 201
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 rArgAlaLeuLeuIleAsnLeuSerLeuGlyPheProGlnArgSerGluAla 80
202 CCCGACCCCAAAAGCTCAAAAGCGCTTTTGGGAAAGCGCAAGGCGG 251
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
81 GluArgGluAlaIleValAspGluMetPheAlaThrAlaProGlnAla 97
252 TTGGAACCTTGCCCGCGCTTTTCAGAAACCGGAAGACATAGAAACAA 301
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
97 tAlaMetAlaIleGluLeuAlaMetArgGlyProLysLysIleGlnGln 114
302 TGTTCAAAGCGGTACACGCGTGGGAAACATGTGCAGCGCTTGGACAA 351
: : : : : : : : : : : : : : : : : : : : : : : : : : :
114 rGValAsp...TrrGlnGlyLeuGluIleIleGlnGluMetArgArgAsn 129
352 CAGGAAGGCGTGTATTCATCAGCGCGCACATGCGCAGCTACGATTTGGG 401
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
130 AspGlnLysValIlePheLeuValProHisGlyTrpGlyValAspLeu 146
402 CGGACGCTACATCAGCAGCAGCGCTCCGCTCCGCTGACGCCCATGTA 451
: : : : : : : : : : : : : : : : : : : : : : : : : : :
146 oAlaMetLeuMetAlaSerGln...GlyLysMetAlaIleAlaMetPheH 162
452 AACCGCGCAAAATCAAAAGCGATGACAAATCATGACGGCGGCGAGGTT 501
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
162 IsAsnGlnGlyAsnProValPheAspTrpIleTrpAsnThrValArg 178
502 CGCGGCAAAAGAAACCGCGCTTACCGCATCAAGGGGTCAACAAAT 551
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 ArgPheGlyArgLeuHisAlaArgAsn...AspGlyLysLeuProH 194
552 CATCAAAACCGCTGCTGCGGCGGAGCAACCATGCTGCTGCC.....G 595
: : : : : : : : : : : : : : : : : : : : : : : : : : :
194 eIleGlnSerValArgGlnGlyTrpGlyTrpGlyTrpLeuProAspGln 211
596 ACCGACGCTCCCTCCCTCCCAAGAGGCGGAGAGCGGATGATGATTTG 645
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 sPHisGlyProGlnHisSerGln.....PheValAspPhe 222
646 TTCGCAAAACCTGCTATACATGACGCTGCGCAAAATTTGCACACGCT 695
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
223 PheAlaThrTrpLysAlaThrLeuProAlaIleGlyArgLeuMetLysVa 239
696 CAAGGCGGTGAAACCGCTGTTTCTGCTGCAAGCGCTG..... 735
239 L.....CysArgAlaArgValIleProLeuP 248

```


Align seg 1/1 to: S07132 from: 1 to: 886

```

51 CATCTCTTGACCCG..... 65
21 HisProthrglyArgThrGlyLeuGlyAspArgLeuLeuIleAlaIle 37
66 .....CCTGCTCAAAATGCTCTCCCTGCGCGCTTCTCTGTCACACG 111
37 tValThrIleAlaIleAlaProIleAlaIleAlaValPheAsnGlnProSerGly 54
112 CTGGCAAAACGGCTCGACATCTGGCTTTACCTTTAAAGAAAGACCG 161
54 laAlaArgAlaPheGlnProMetThrAlaIleProThrGlnGlyAlaArg 70
162 CGC.....GGCAATGCTCG 175
71 ArgIleAlaProAlaIleGlyLeuGlnAsnLeuLeuAlaIleArgIle 87
176 CCAATATGCGTCAGCAGCATGAATCCGACCCCAAAACGGTCAAAAGCC 225
87 nGlyPheLeuAspGlyArgGlyAspGlnArgAlaGlnProAlaGlnAlaG 104
226 GTTTTGGCGAAACGGCAAAAGCGCTTGGAACTGGCCCGCTTTT 275
104 lYArgAlaGlyHisGlyArgArgGlyArgArg..... 115
276 CAGAAACCGGAAAGCATAGAAACAT..... 302
116 ArgArgGlyGlyArgArgArgArgGlyGlyArgPheLeuLeuGlyLe 132
303 .....GTTCAAACGGGTACACGGCTGGAAACATGTGCAGCAG 339
132 uValAlaArgProAlaGlyArgGlyGlnThrLeuGly.....ProAlaG 147
340 GCTTGGCAAAACAGA..... 356
147 lYSerGlyLysIleArgGlyGlnProPheLeuArgArgIleAlaIleGln 163
357 .....AGGCTGCTATTCATCAGCCGCG 379
164 lIleGlnGlyLysPheGlyHisPheArgSerAlaValAlaThrGlyGln 180
380 ACATCG.....CAGC 390
180 nHisGlnMetProIleAlaIleAlaLeuAlaGlyValLeuAspGlyPheGln 197
391 TACGATTTGGCGGAGCTACAT...CAGCCGACGCTTCCCTCCCT 437
197 rGArgArgGlyArgGlyGlnHisGlyGlyLysAlaIleAlaGlyAla 213
438 GACCGC...CATGTACAAACCGCGAAATCAAGC..... 470
214 AspHisGlyHisValAlaGlyAlaIleArgHisAlaLeuLeuPheGln 230
471 .....GATAGCAAAATCATCAGCGCGGCGAG 498
230 uGlyAlaValAlaPhePheIleAspAspArgGlnAlaGlnIleGlyIleG 247
499 GTTCCGGCAAGAAAGAAACCGCGCTACACATACAGGGGTCAAAAG 548
247 lYglnLysIleArgArgSerArgProHisHisArgArg..... 260
549 AATCATCAAGCGCTGCTGGCGGCAACCATGCTGCTGCCGAGC 598
261 .....ProGlnGly.....HisArgProProSerPr 270
599 AGCTCC.....CTCCCTCAAGAAAGCGGCGA. 626
270 oProProArgArgArgAlaHisLeuArgMetProLeuHisArgSerGlyA 287
627 .....AGCGTATGCGGTGA..... 641
287 lAGlnAlaValAlaGlyAlaIleProArgProLeuGlyGlnGlyAspPhe 303

```

```

641 ..... 641
304 GlyGlnGlnHisGlnSerLeuProProAlaIleAlaGlnGlyPheGlyAspArg 320
642 .....TTTCTTGGC 651
320 gLeuGlnIleAspLeuGlyLeuAlaArgAlaGlyAspProPheGlnGln 337
652 AAACCTGCCATATCCATGACCGTGGCGCAAA..... 683
337 lInThr.....GlyLysSerLeuValLysArgArg 346
684 .....ATTGGACACGTCAAGGCTGA 706
347 AlAGlnAlaValArgArgArgLeuLeuIleGly...ArgGlnGlnArgSe 362
707 AAACCTGTTTCTG.....CTGGCAACGGCTGCTGGCGGACAAAGT 750
362 rGlyProValGlyIleGlyLeuArgArgProPheIleArgThrGlyN 379
751 TTCGATTTCACATCCG.....CCCGTCA 776
379 lSArgLeuGlnGlnProGlyLeuGlyHisArgArgHisArgArgPro 395
777 AGGGGA..... 782
396 HisGlyArgPheProArgGlnIleGlyAlaGlyGlyGlnThrGlyN 412
783 .....ATTGAACGGGCAAAACCATGATGCCGCTGTTCACAGCGCA 827
412 tValValLysAsnArgGlnAsnProLeuAlaIleAlaGlnProArg 428
seq_name: p1r2:C75580

```

```

seq_documentation_block:
adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: AF5250; M01D:20036896
A:Accession: C75580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <WHI>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12376.1; PID:g646
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0268
A:Map position: 2

```

```

alignment_scores:
Quality: 116.00 Length: 268
Ratio: 0.906 Gaps: 13
Percent Similarity: 47.761 Percent Identity: 26.866

```

alignment_block:

US-09-303-518D-569 x C75580 ..

Align seg 1/1 to: C75580 from: 1 to: 376

```

60 GACCGCCCT...GCTCAATGCCCTCCCTGCGCGCTTCTCTGCTGC 106
|||||
120 AspArgProThrPValSerArgArgLeuArgAlaIleAlaIleArgLeuAlaIle 136
107 ACACGCTGGCAAAACGGCTCGACATCTGGCTTTTACCTTTAAAGAA 156
|||

```



```

136 r.....LeuArgGlyAlaGlyAsnLeuArgGlyArgG 148
157 GACCGCGCCGATGTCGACCATATGCGACGAGCGCATGATCCGA 206
148 LysSerAlaAlaArgArgArgAlaProProAlaArgTpaArgG 164
207 CCCCMAAGGTCMAAGCGTTTTCGGAAGCGCAAGCGGTTTG 256
165 ProArgAlaArgLeuGlyArgGlyHisLeuArgSerAlaArgAla 181
257 AACTGGCCCCGGTTTTCAGAAACCGAAGCATAGAACATGTTTC 306
181 ahisAlaProAlaProAlaSerArgProAlaArgHisArg..... 193
307 AAAGCGGTACACGCGTGGGAACATGTGACAGCGTTTGACAAACGA 356
194 .....AlaCysGlyAlaGlyHisArgG 201
357 AGGCTGCTATTATCATCAGCCGACATCGGACGTACGATTGGCGGAC 406
202 ArgProAla.....GlyArgArgArgProLeuArgAlaArgArg 215
407 GTCACAT...CAGCGACAGCTTCGCTCCGCTGACCGCATGTACAAA 453
215 lValGlyLeuLeuAspValGlyGlnArgProAlaArgArgHis..... 229
454 CCGCCGMAATCAAGCGATAGACAAATCATGACAGCGCGGCGGTTG 503
230 ..ProGlyHisGlnHisSerAlaArgArgAlaSerGlyGlyProAlaArg 245
504 CGGCAAGGMAAACCGCGCTACCGCATACAGCGGTCAACAAATCA 553
246 ArgGlnArgArgGlyProAla.....ArgGlyGlySerGlyAl 258
554 TCAAGCGCTGCTGCGGCGGGAAGCAACCATGCTGCGCGCA..... 596
258 aArgThr.....AlaArgArgArgHisArgProGlyArgGlyAla 272
597 .....CCAGTCCCTC.....CCC 611
272 TGGlProArgAlaValAlaProAlaLeuArgGlySerAspArgPro 288
612 TCAGAGAGCGGGAAGCGGTATGCGATTCTTTCGCAACCTGCT 661
289 AlaserGlyArgGlyArgArgCysProGly..... 298
662 ATACCATGCGCTGCGCGCAAAATTGSCACAGTCMAAGCGGTGAAAAC 711
299 .ProGlyAspGlyGlyAlaLeuAlaGly..... 308
712 CTGTTTTCGCTGCGGACGCTGCTGCGGACAGATTTCGATTGCA 761
309 .....LeuHisLeuAlaLeuSerArgHisHisProGlyHisSer 321
762 CATCGCGCCCGTCAGAGGGAATTGAACGGCGACAAAGCCCATGATGCG 811
332 ArgProGlyArgAspSerGlyAlaGlnAlaAspAlaAlaArgProAla 338
812 CCGT 815
338 gArg 339
seq_name: p1r2:E86965
seq_documentation_block:
conserved_hypothetical_protein_MU0453 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E86965
R:Coyle, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001

```

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: E86965
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <STO>
A:Cross-references: GB:AL450380; NID:g13092692; PIDN:CMC29961.1; GSPDB:GN00147
A:Gene: MU0453

alignment_scores:
Quality: 115.50 Length: 253
Ratio: 0.808 Gaps: 14
Percent Similarity: 56.522 Percent Identity: 28.063

alignment_block:
US-09-303-518D-569 x E86965 ..
Align seg 1/1 to: E86965 from: 1 to: 320

```

75 ATGCTCTCCCTGCTGCGGCTTC...CTGTCGACACGCTGGAAAC 121
||||| ||||| ||| ..... |||
37 MetProGluSerAlaAlaArgPheAlaPheAsnThrGlyAlaArgTyrAl 53
122 GGCTGGACATCTGGCGTTTACCTTTAAAGAGACCGCGCGCATC 171
||||| ..... |||
53 aaAlaArgAsnGlyGlyProAspGlnLeuArgGlyAsnLeuAlaArgGly 69
172 GTGCGCAATATGCGTCAGCGACGATGAATCCGACCCCAAAAGGTCA 221
70 lIleGly.....ValGlnAlaAlaAspValProAsp..AlaLeuIleAr 83
222 AGCGCTTTTTCGGAAGCGCAAAAGCGGTTTGGAACTTCCCGCGGT 271
...: ..... |||
83 gThrSerLeuAlaSerTyrAlaArgTyrTpaArgGlyAla..... 96
272 TTTTCAAGAAACCGGA...GACATAGAAACATGTTCAAGCGTACAC 318
||||| ||| ...: ..... |||
97 ..PheArgLeuProThrMetAsnProHisThrValAlaIleValGly 112
319 GGCTGG.....GAACATGTGACGAGGCTTGGCAAAACGCA 356
...: ..... |||
113 AlaTyrGlyIleAspLeuHisArgValGlyGlyAlaLeuSerAlaGlyAr 129
357 AGCGCTGATTCATCAGCGCGCACATCGGACGATTTGGCGCGAC 406
...: ..... |||
129 gGlyValAlaLeuAlaLeuProHisSerGlyAsnThrAspMetAlaGly 146
407 GTCATCATGCGAG...CAGCTTCGCTCCCGCTGACCGCC...ATGTAC 450
...: ...: |||
146 alThrPheValGlnCysHisGlyThrPheThrThrValAlaGluArgLeu 162
451 AAACCGCGGAATTC.....AAAGCATAGACAAATTCATGACGCGG 494
||||| .....: |||
163 LysProGluSerLeuTyrArgArgPheIleAsnTyrArgGlnHisLeuG 179
495 C...AGGTTGGCGGCAAGGMAAACCGCGCTACGACGATCAAGGG 541
...: .....: |||
179 yPheGlyValLeuProMetSerAlaAsnLysAspThrGlyPheGlnAla 196
542 TCAACAAATCATC...AAAGCGCTGCGGCGGCGGACGACCATGCTG 588
...: .....: |||
196 eupHleuLeuLeuGlyGlyArgLeuArgSerHisnArgValGlyCysLeu 212
589 CTGCGCCACACGTCCTCCCTCAAGAAAGCGGGAAGCGGTATGGT 638
...: .....: |||
213 MetAlaGluArg.....AspLeuThrArgThrGlyValGlyAla 225
639 GGATTTCTGCGCAACCTGCTATACATGACGCTGCGGCGGCAAAATTCG 688
||||| .....: |||
225 lAspPhePheGlyGluProThrArgMetProAlaGlyProAlaLysLeu 242

```

